

## (12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
8 July 2004 (08.07.2004)

PCT

(10) International Publication Number  
WO 2004/057018 A2

(51) International Patent Classification<sup>7</sup>: C12Q 1/00

(21) International Application Number: PCT/CH2003/000836

(22) International Filing Date: 19 December 2003 (19.12.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data: 10/324,967 20 December 2002 (20.12.2002) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:  
US 10/324,967 (CON)  
Filed on 20 December 2002 (20.12.2002)

(71) Applicant (for all designated States except US): UNIVERSITY OF GENEVA [CH/CH]; 15, rue Lombard, CH-1205 Geneva (CH).

(72) Inventors; and

(75) Inventors/Applicants (for US only): COSSON, Pierre [FR/CH]; 55, chemin Poluzzi, CH-1227 Carouge (CH). KÖHLER, Thilo [CH/CH]; 15, rue de la Tambourine, CH-1227 Carouge (CH). BENGHEZAL, Mohammed [CH/CH]; 8A, chemin des Fins, CH-1218 Grand-Saconnex (CH). MARCHETTI, Anna [CH/CH]; 36, avenue

(74) Agent: E. BLUM & CO.; Vorderberg 11, CH-8044 Zürich (CH).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

## Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: VIRULENCE GENES, PROTEINS, AND THEIR USE

(57) Abstract: A series of genes from *Pseudomonas aeruginosa* and *Klebsiella* are shown to encode products that are implicated in virulence. The identification of these genes therefore allows attenuated microorganisms to be produced. Furthermore, the genes or their encoded products can be used to identify antimicrobial drugs, diagnostic methods for the identification of a pathogen-associated disease, and in the manufacture of vaccines.

WO 2004/057018 A2

## VIRULENCE GENES, PROTEINS, AND THEIR USE

### FIELD OF THE INVENTION

This invention relates to virulence genes and proteins, and their use. More particularly, it relates to genes and proteins/peptides obtained from gram-negative bacteria,  
5 and their use in therapy and in screening for drugs.

### BACKGROUND OF THE INVENTION

According to health care experts, infectious diseases caused by microbes are responsible for more deaths worldwide than any other single cause. The current estimate of the annual cost of medical care for treating infectious diseases in the United States alone is  
10 about \$120 billion. While antibiotic treatment is effective for many microbial infections, antibiotic resistance among pathogenic bacteria is a growing health concern. Indeed, the American Medical Association has concluded that, "the global increase in resistance to antimicrobial drugs, including the emergence of bacterial strains that are resistant to all available antibacterial agents, has created a public health problem of potentially crisis  
15 proportions."

*Pseudomonas* and *Klebsiella* are two genera of gram-negative bacteria that pose a significant health risk to infected host organisms, in part, due to their resistance to many antibiotics. These bacteria are noted for causing life-threatening infections, particularly in the lung. Cancer and burn patients also commonly suffer serious *Pseudomonas* infections, as do  
20 certain other individuals with immune system deficiencies. While *Klebsiella* sp. is responsible for many types of infections, outside of a medical setting, the most common infection caused by *Klebsiella* bacteria is pneumonia.

There is a need in the art for new antimicrobial therapeutic strategies.

## SUMMARY OF THE INVENTION

The present invention is based, in part, on the discovery of 46 genes, when mutated lower the virulence of a gram-negative bacterium, and can be used in new antimicrobial therapeutic strategies. The invention provides attenuated bacterial mutants that are derived 5 from pathogenic strains. These attenuated bacterial stains have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, 10 VIR44, VIR45, and VIR46; and show reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism. The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism. The term, "mutant," as used herein, 15 an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene.

The invention also provides attenuated bacterial mutants that are derived from pathogenic gram-negative bacterial strains. These attenuated gram-negative bacterial strains 20 have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and show reduced inhibition of 25 *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene. It is also preferred that the attenuated gram-negative bacterial mutant be derived from a *Pseudomonas* or *Klebsiella* spp. It is more preferred that the attenuated gram-negative bacterial mutant is a strain of *P. 30 aeruginosa* or *K. pneumoniae*.

The invention additionally provides for a VIRX gene that may be part of an operon. The term, "operon," as used herein, is a unit of bacterial gene expression and regulation

comprising several genes, usually with complementary functions. Insertion in a gene in an operon typically interferes with the function of this gene and of other genes located downstream or upstream in the operon. The function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon. Accordingly,

5 the invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, 10 VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation.

15 The invention provides for one or more of the following attenuated *Pseudomonas* mutant strains: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19. The invention also provides for one or more of the following attenuated *Klebsiella* mutant strains: MUT20; MUT21; MUT22; MUT23; MUT24; MUT25; MUT26; MUT27; 20 MUT28; MUT29; MUT30; MUT31; MUT32; MUT33; MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43; MUT44; MUT45; and MUT46.

The invention additionally provides a method for identifying an antimicrobial drug, wherein a candidate composition is contacted with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, 25 VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46. The biological activity of polypeptide in the presence of the candidate composition is compared with the biological activity of the 30 polypeptide in the absence of the candidate composition. Alteration of the biological activity of the polypeptide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate

composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be, *e.g.*, an immunoglobulin, polysaccharide, lipid, nucleic acid, or combination thereof.

The invention additionally provides a method for identifying an antimicrobial drug, 5 wherein a candidate composition is contacted with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, 10 VIR42, VIR43, VIR44, VIR45, and VIR46. The expression of the polynucleotide in the presence of the candidate composition is compared with the expression of the polynucleotide in the absence of the candidate composition. Alteration of the expression of the polynucleotide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate 15 composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be a polypeptide, polysaccharide, lipid, nucleic acid, *e.g.*, ribonucleic acid, or combination thereof. In a preferred embodiment, the ribonucleic acid of the candidate composition is a small interfering ribonucleic acid.

20 The invention additionally provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, 25 VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second subject known not to have the presence of the pathogen, wherein an alteration in the 30

expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

5 The invention also provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, 10 VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polynucleotide in the sample of step (a) to the amount of the polynucleotide present in a control sample from a second subject known not to have the presence of the pathogen, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

20 The invention additionally provides attenuated bacterial strains that can be used as vaccines and as vectors for foreign antigens and for foreign DNA. These attenuated bacterial strains are useful for the preparation of vaccines effective against diseases associated with the corresponding bacterial strains. In a preferred embodiment, the attenuated bacterial strains are derived from *Pseudomonas* or *Klebsiella* spp.

25 The invention additionally provides attenuated bacterial strains that can be used as vectors for foreign genes cloned from other pathogens that will be expressed into proteins, and will raise protective immune responses against the pathogens from which they are derived. In a preferred embodiment, the attenuated bacterial strains used as the vectors are derived from *Pseudomonas* or *Klebsiella* spp.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

### **DETAILED DESCRIPTION OF THE INVENTION**

The present invention is based, in part, on the discovery of 46 genes when mutated lower the virulence of a gram-negative bacterium. Nineteen of these virulence genes were identified in *P. aeruginosa* PT894, while the remaining 27 genes were derived from mutagenesis of *Klebsiella*. These bacterial mutants have attenuated virulence relative to isogenic bacterial strains and are designated "MUTX." Provided herein are virulence genes affected in each novel, attenuated MUTX strain, as well as the nucleotides and polypeptides encoded thereby. The sequences encoded by the affected genes are collectively referred to as "VIRX nucleic acids" or "VIRX polynucleotides" and the corresponding encoded polypeptides are referred to as "VIRX polypeptides" or "VIRX proteins." Unless indicated otherwise, "VIRX" is meant to refer to any of the novel sequences disclosed herein.

The peptides and genes of the invention are useful for the preparation of therapeutic agents to treat infection because they attenuate the virulence of the wild-type pathogen. Therapy can be preventative or therapeutic. A subject receiving therapy can be, e.g., a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

#### **I. IDENTIFICATION OF *PSEUDOMONAS* AND *KLEBSIELLA* GENES ENCODING VIRULENCE FACTORS**

Genes encoding virulence factors (e.g., pathogens or toxins) to a host organism were

identified by comparing the growth of *Dictyostelium discoideum*, in the presence and absence of test mutants of *Pseudomonas* and *Klebsiella* with an identifiable genetic alteration as detailed in International Application PCT/IB02/03277, filed June 7, 2002. *Dictyostelium* amoebae feed phagocytically upon bacteria such as *K. pneumoniae*. When *Dictyostelium* cells are plated with *K. pneumoniae* bacteria, each amoeba creates a plaque in the bacterial lawn in the region where bacteria have been phagocytosed. Addition of pathogenic bacteria, e.g., *P. aeruginosa* strain PT894 to the lawn of *K. pneumoniae* bacteria, inhibits the growth of the amoebae.

*Pseudomonas* test mutants were made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (see, PCT/IB02/03277, filed June 7, 2002). *Klebsiella* mutants were also made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (see, PCT/IB02/03277, filed June 7, 2002) using the *PHG1a* mutant *Dictyostelium* strain (Cornillon *et al.*, J. Biol. Chem., 275(44): 34287-92, 2000), a strain which was found to be particularly sensitive to virulent bacteria. Specifically, the *Klebsiella* mutants were obtained by standard bacteria electroporation technique using the plasposon pNKBOR (Genbank accession number: AF310136) and selected on solid LB medium containing 50 µg/ml kanamycin (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Other mutagenesis methods known in the art, e.g., ultraviolet radiation exposure, treatment with intercalating agent or transducing phage, may also be used to generate mutants. Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced virulence were subsequently identified and characterized by techniques well known in the art. Identification of specific gene mutations in *Klebsiella* mutants was performed by plasmid rescue and cloning of the genomic DNA at the insertion site mutant using the BglII or ApaI restriction enzyme according to (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Identification of specific gene mutations in *Pseudomonas* mutants was performed by subcloning the transposon and surrounding bacteria genomic DNA into an acceptor plamid. DNA sequencing was performed on amplified rescued plasmids, in order to identify the insertion site of the transposon. Rat mortality assays such as that described by Join-Lambert *et al.*, Antimicrob. Agents Chemother., 45(2): 571-6, 2001, can be used to

corroborate attenuated virulence activity in a mammalian host.

The 19 *Pseudomonas* attenuated MUTX organisms harboring the VIRX genes are summarized below in Table 1.

Table 1

STRAIN	AFFECTED VIRULENCE GENE(S)	REFERENCE
MUT1	anthranilate phosphoribosyltransferase (trpD; PA0650)	Essar <i>et al.</i> , J. Bacteriol., 172:853-66, 1990; Essar <i>et al.</i> , J. Bacteriol., 172:867-83, 1990.
MUT2	ATP sulfurylase small subunit (CysD; PA4443)	Leyh <i>et al.</i> , J. Biol. Chem., 263:2409-16, 1988; Hummerjohann <i>et al.</i> , Microbiology, 144 (Pt 5):1375-86, 1998
MUT3	CysQ (PA5175)	Peng and Verma, J. Biol. Chem., 270:29105-10, 1995; Neuwald <i>et al.</i> , J. Bacteriol., 174:415-25, 1992.
MUT4	D-amino acid dehydrogenase, small subunit (dadA; PA5304)	Lobacka <i>et al.</i> , J. Bacteriol., 176:1500-10, 1994.
MUT5	imidazoleglycerol-phosphate synthase, cyclase subunit (hisF1; PA5140)	Fani <i>et al.</i> , Mol. Gen. Genet., 216:224-9, 1989; Fani <i>et al.</i> , Mol. Gen. Genet., 216:224-9, 1989.
MUT6	N-acetyl- $\gamma$ -glutamyl-phosphate reductase (ArgC; PAO 0662)	Smith <i>et al.</i> , Gene, 49:53-60, 1986.
MUT7	Dihydrolipoamide acetyltransferase (AceF; pyruvate dehydrogenase complex component E2; PA5016)	Rae <i>et al.</i> , J. Bacteriol., 179:3561-71, 1997.
MUT8	NADH dehydrogenase I chain H (nuoH; PA2643)	Weidner <i>et al.</i> , J. Mol. Biol., 5:233:109-22, 1993; Weidner <i>et al.</i> , J. Mol. Biol., 233:109-22, 1993.
MUT9	pyoverdine synthetase D (PvdD; PA2399)	Rombel <i>et al.</i> , Mol. Gen. Genet., 246:519-28, 1995; Merriman <i>et al.</i> , J. Bacteriol., 177:252-8, 1995.
MUT10	RND multidrug efflux transporter MexD (mexD;PA4598)	Poole <i>et al.</i> , Mol. Microbiol., 21:713-24, 1996; Poole <i>et al.</i> , Mol. Microbiol., 21:713-24, 1996.
MUT11	PA3721	Stover <i>et al.</i> , Nature, 406:959-964, 2000.
MUT12	PA0596	Tan <i>et al.</i> , Proc. Natl. Acad. Sci. USA, 96:2408-13, 1999.
MUT13	PA5265	Stover <i>et al.</i> , Nature, 406: 959-964, 2000.

MUT14	pyochelin biosynthetic protein pchC (PA4229)	Serino <i>et al.</i> , Mol. Gen. Genet., 249: 217-28, 1995; Serino <i>et al.</i> , J. Bactiol., 179:248-57, 1997
MUT15	dihydroaeruginoic acid synthetase (pchE; PA4226)	Reimann <i>et al.</i> , Microbiology, 144: 3135-48, 1998.
MUT16	Pyochelin synthetase (pchF; PA4225)	Reimann <i>et al.</i> , Microbiology, 144: 3135-48, 1998.
MUT17	ATP-binding component of the ABC transporter (pchH; PA4223)	Featherston <i>et al.</i> , Mol. Microbiol., 32(2):289-99, 1999; Reimann <i>et al.</i> , J. Bacteriol., 183:813-20, 2001.
MUT18	ATP-binding component of the ABC transporter (pchI; PA4222)	Reimann <i>et al.</i> , J. Bacteriol., 183:813-20, 2001.
MUT19	putative O-antigen biosynthesis gene cluster	Rocchetta <i>et al.</i> , Microbiol. Mol. Biol. Rev. 63:523-53, 1999.

The 27 *Klebsiella* attenuated MUTX organisms harboring the VIRX genes disclosed in the present invention and assigned a new role in virulence are summarized below in Table 2.

Table 2

STRAIN	AFFECTED VIRULENCE GENE(S)
MUT20	hypothetical transcriptional regulator in met G-dld intergenic region
MUT21	$\beta$ -cystathionase
MUT22	ribosome binding factor A
MUT23	aspartokinase/homoserine dehydrogenase
MUT24	cystathionine $\gamma$ -synthase
MUT25	Phosphoribosylformylglycinamidine synthase

MUT26	homoserine transsuccinylase
MUT27	3'-phosphoadenosine 5'-phosphosulfate reductase
MUT28	Sfi protein
MUT29	transcriptional activator protein LysR
MUT30	TrpD
MUT31	N-acetylglucosamine-6-phosphate deacetylase
MUT32	WaaQ
MUT33	2-Isopropylmalate synthase
MUT34	histidinol dehydrogenase
MUT35	UDP-galactopyranose mutase
MUT36	O-antigen export system permease protein rfbA
MUT37	uridyltransferase
MUT38	pyridoxine phosphate biosynthetic protein PdxJ-PdxA
MUT39	triose phosphate isomerase
MUT40	aldehyde dehydrogenase
MUT41	galactosyl transferase
MUT42	siroheme synthetase
MUT43	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
MUT44	glucose-6-phosphate isomerase
MUT45	DNA methylase
MUT46	putative inner membrane protein

## II. ATTENUATED BACTERIAL MUTANTS

### A. Attenuated *Pseudomonas aeruginosa* Mutants

#### MUT1

A *Pseudomonas* bacterial mutant (MUT1) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding anthranilate phosphoribosyltransferase (PA0650). This gene encodes the VIR1 nucleic acid (SEQ ID NO:1) shown in Table 3A.

10

**Table 3A. VIR1 Nucleotide Sequence (SEQ ID NO:1)**

```

ATGGATATCAAGGGAGCCCTCAATCGCATCGCAACCAGCTGACCTGACCACCGAGGAATGCAGG
CGGTCAATGCCAGATCATGACCGGGCAGTCACCGACCGCAGATCGGCGCTTCCCTGATGGGCAT
CGGGATGAAGAGCGAAACCATCGACGAGATCGTCGGCGGGTGGCGGTGATGCGCGAACTGGCCGAC
GGCGTGCAGTTGCCTACGCTGAAGCATGTGGTCACGTTGGCGGGCAGGGCGATGGCGCGAAC
TCTCAACGTGTCCTCGCGCGTCCTTCGTTGTCGCCCGCTGGCGGCAAGGTGCGCAAACACGG
TAACC CGCGCGTCTCGCGCAAGAGCGGCAGCGCCGACTTGCTGGAAAGCGCCGGCATCTACCTGGAG
CTGACCTCCGAACAGGTGGCGCGTTGCATCGACACCCTGCGCTGGGTTCATGTTCGCCCAGGTCC
ACACAAAGGCAGATGAAGTACGCCGCCGGTCCCGCCGCGAGCTGGGCTTGGGACTCTGTTAACAT
GCTGGGCCACTGACCAACCGGGAGTCAGGCACCAAGGTGGTCCGGGTGTCACCCAGGAAC
TGCAAGGCCCTGGCTGAAGTGCTCAAGCGTCTCGGCAGCGAGCATGTGCTGGTGGTGCATTGCGCG
ACGGGCTGGACGAGTTCACTGCTGGCCGGCAGCCACATTGCCGAGTTGAAGGACGGCAGGGTACG
CGAGTACGAAGTGGCTCCGGAGGACTTCGGGATCAAGAGGCCAGACCCCTGATGGGCTGGAGGTGAC
AGTCCGCAGGCCCTGGCTGGAACTGATCCGCAGCCTGGGGCGGCAAGACCGAGGCTGGGAGA
AGGCCGCCGAGCTGATCGTGAATGCCGGCCGGCAGTGTACGCTGCCGATCTGGCACCAGCCT
GCACGAGGGCATTCAACTGGCCCACGATGCCCTGCACACCGGGCTGGCACGGGAGAAGATGGACGAA
CTGGTGGCCTTCACCGCCGTTACAGAGAGGAGAACGACAGTGA

```

The VIR1 protein (SEQ ID NO:2) encoded by SEQ ID NO:1 is presented using the one-letter amino acid code in Table 3B.

**Table 3B. Encoded VIR1 protein sequence (SEQ ID NO:2)**

```

MDIKGALNRIVNQLDLTTEEMQAVMRQIMTGQCTDAQIGAFLMGMRMKSETIDEIVGAVAVMREL
ADGVQLPTLKHVVDVVGTDGANIIFNVSSAASFVVAAGGKVAHKGNRAVSGKSGSADLLEAAG
IYLELTSEQVARCIDTVGVGFMAQVHHKAMKYAAGRRELGLRTLNFNMLGPLTNPAGVRHQVVG
VFTQELCKPLAEVLKRLGSEHVLVVSNDLDEFSLAAATHIAELKDGEVREYEVRPEDFGIKSQ
TLMGLEVDSPQASLELIRDALGRRKTEAGQKAAELIVMNAGPALYAADLATSHEGIQLAHDALH
TGLAREKMDDELVAFTAVYREENAQ

```

15

The role of VIR1 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

**MUT2**

A *Pseudomonas* bacterial mutant (MUT2) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the ATP sulfurylase small subunit (CysD; PA4443). This gene encodes the VIR2 nucleic acid (SEQ ID NO:3) shown in Table 4A.

**Table 4A. VIR2 Nucleotide Sequence (SEQ ID NO:3)**

```

ATGGTCGACAAACTGACCGACCTGAAACAGCTGGAGGCCGAAAGCATCCACATCCCGAGGTGG
CCGCCGAGTCGATAACCGGTGATGCTGTACTCGATCGGCAAGGATTCCCGGTCATGCTGCACCT
GGCCCGCAAGGCCCTCTCCCCGGCAAGCTGCCCTCCCGGTGATGCACGTGGACACCCGCTGGAAA
TTCCAGGAGATGTACAGGTTCCGTATCGGATGGTCGAGGAATGGGCTGGATCTGATCACCCACG
TCAACCCGGACGGCGTCGCCAGGGCATCAACCCGTTCACCCACGGCAGCGCCAAGCACACCGACGT
GATGAAGACCGAGGGACTCAAGCAGGCCCTGACAAGTACGGTTCGACGCTGCCTCGGCCGTGCG
CGCCCGCACGGAGGAAGTCGCGGCCAAGGAACGGGTCTATTGTTCCGCGACAGCAAGCACCGCT
GGGACCCGAAGAACCGCGTCCCGAGCTGTGAAACATCTACAACGCGAAGGTGAAGAACGGCGAGTC
GATCCCGCTCTCCCGCTGTCCAACCTGGACCGAGCTGGACATCTGCGAATACATCTACCTGGAAAGC
ATCCCGATCGTCCCCTGTACTTCGCGCCGGAGCGCGAGGTCATCGAGAAGAACGGCACATTGATCA
TGATCGACGACGAGCGCATCCTCGAGCATCTCTGACGAAGAACGGCGCATCGAGAACGCGCAT
GGTGCCTCCGTACCCCTCGGCTGCTACCGCTCACCGCGCGTCAAGCAGCGCCACCACGCTG
CCGAAATCATCCAGGAAATGCTCTGACGCGTACTTCCGAACGCCAGGGCGGGTCATCGACCATG
ACCAGGCCGGTTCGATGGAAGAAAAGAACGTCAGGGCTATTCTGA

```

10

The VIR2 protein (SEQ ID NO:4) encoded by SEQ ID NO:3 is presented using the one-letter amino acid code in Table 4B.

**Table 4B. Encoded VIR2 protein sequence (SEQ ID NO:4)**

```

MVDKLTHLKQLEAESIHIIREVAAEFDNPVMLYSIGKDSAVMLHLARKAFFFPGKLPFPVMHVDTR
WKFQEMYRFRDRMVEEMGLDLITHVNPDGVAQGINPFTHGSAKHTDVMKTEGLKQALDKYGFDA
FGGARRDEEKSRAKERVYSFRDSKHRWDPKNQRPELWNIYNGVKKGESIRVFPLSNWTELDIWO
YIYLEGIPIVPLYFAAEREVIEKNGTLIMIDDERILEHLSDEEKARIEKRMVRFRTLGCYPLTGA
VESSATTLPETIQEMILLRTSERQGRVIDHDQAGSMEKKRQGYF

```

The role of VIR2 in virulence was confirmed using phage to retransduce this mutation

15 into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

**MUT3**

A *Pseudomonas* bacterial mutant (MUT3) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding CysQ (PA5175). This gene encodes the VIR3 nucleic acid (SEQ ID NO:5) shown in Table 5A.

5

**Table 5A. VIR3 Nucleotide Sequence (SEQ ID NO:5)**

```
ATGAGGCCGGTGCCTGGGGCGAATTGGTGGCCTGGTGCAGGCGATCCCTGCCGC
ACTGGCGCGCCGACGTGGTGGCGCTCGAAGGCCGACGAATGCCGGTGACTGCCGCCACCTGGC
CGCGCACCATATATTGGAGGCCGGATTGCGGGCGCTGCCGCCGACATTCCGGTGCTTCCGAAGAG
GATTGCGAGATACCGCTGAGCGAGCGCCACTGGCGCGCTGGCTGGCTGGACCCGCTGGACCG
GCACCAAGGAGTTCATCTCCGGTAGCGAGGAGTTACCGTCAACGTGGCCCTGGTCGAGGATGGCCG
GGTGGCTGTTGGGCGCTGGTGGCGTGCCGGTGAGCGGCCGCTGCTACTACGGTGGCGCCGGTCTGGT
GCCGGCGAGGAGGCCGATGGCCGCGCGCAACCGATAGTGTGGCCTGGAGGCCGAGGAGGCCT
TCACCGTGGTGGCCAGCAAGCGCCATGGCAGCCGGCCAGGAGGCCCTGGATGGCTTGAGCGA
GCGCTTCGGCGACCTGCGCGAGCCAGCAGCATCGGCAGTTCGCTGAAGTTCTGCCTGCTGGCCGAGGGC
GCTGCCGACTGCTATCCCGCCTGACGCCAACCTCGCAATGGACACGGCCGCCGCCAGGGTGTGC
TGGAAAGGCGCCGGCGCCGAGGTGCTGACCTGCAATGGTGCGCCATTCACCTACGAGCCGCGAGGA
TTACCTCAACGGCTCCTGGCCCTGCGCGCCGCCGAGTGGCGCAGCGAGCTGATCCAACTG
GCGCGCGCTGCACTGA
```

The VIR3 protein (SEQ ID NO:6) encoded by SEQ ID NO:5 is presented using the one-letter amino acid code in Table 5B.

**Table 5B. Encoded VIR3 protein sequence (SEQ ID NO:6)**

```
MRPVPWGELVALVRRAGEAILPHWRADVVVRSKADESPVTAADLAHHILEAGLRALAPDIPVLS
EEDCEIPLSERGHWRWWLVDPLDGTKEFISGSEEFVNVALVEDGRVLFGLVGPVSGRCYYGG
AGLGAWREADGRAQPISVRLEPEEAFTVVASKRHGSQPAQERLLDGLSERFGDLRRASIGSSLKF
CLLAEGAADCYPRLPTSQWDTAAQGVLEGAGGEVLDLHGPFTYEPREDYLNGSFLALPRAAE
WRSELIQLARALH
```

10

#### MUT4

A *Pseudomonas* bacterial mutant (MUT4) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding D-amino acid dehydrogenase, small subunit (dadA; PA5304). This gene encodes the VIR4 nucleic acid (SEQ ID NO:7) shown in Table 6A.

**Table 6A. VIR4 Nucleotide Sequence (SEQ ID NO:7)**

```
ATGCGAGTTCTGGTCCTGGCAGCGGTGTCATCGGTACCGCCAGTGGCTATTACCTGGCCCGTGCCG
GGTCGAGGTGGTGGTGGCGACCGTCAGGACGGTCCCGCGCTGGAAACCAAGCTTCGCCAACGCCGG
```

```

CCAGGTGTCTCCCGCTACGCTTCGCCCTGGCAGCCCCGGGCATTCCCCTGAAGGCCATGAAGTGG
CTGCTGGAAAAGCACGCCGCTGCCATCAAGCTCACCTCGATCCCAGCCAGTACGCCCTGGATGC
TGCAGATGCTGCGCAACTGCACCGCCGAGCGCTACGCCGTAAACAAGGAGCGCATGGTCCGCTGTC
CGAGTACAGCCCGATTGCCCTGACGAACCTGCCGAGACCGGCATGCCCTACGAGGGCCGCACC
CTCGGCACCAACCCAACTGTTCCGACCCAGGCCAGCTGGACGCCGGCAAGGACATGCCGTGC
TCGAGCGCTCGGCCTACGAGGTTCTGACCGCAGCGCATGCCCGCTAGAGCCGGCTT
GCCAAGGTGCCGACAAGCTGGTCGGCCCTGCGCCCTGCCAACGACCAGACCGGCAGTGCCAG
CTGTTACCAACCCGCTGGAAATGGCAAGGGCTGGCGTGGAGTTCCGCTTCGGCCAGAACAA
TCGAGCGCTGGACTTCGCCGGCAGCCGATCAACGGCGTGTGGTCAACGGGAATTGCTCACCGC
CGACCAACTACGTGCTGGCCCTGGCAGCTACTGCCGCAACTGCTCAAGCGCTGGGTATCAAGGCT
CGGGTCTATCCGCTGAAGGGTTATCGCTGACCGTGGCCGATACCAACCCGGAGATGGCGCCGACCT
CGACCATCCCGACGAGACCTACAAGGTGGCGATCACCCGCTTCGCGCAGCGCATCCGCTGGCGG
CATGGCGAAATGCCGGCTTCGACCTGTCGTGAACCCCGCCGGCAGACCCCTGGAAATGATC
ACCACCGACCTCTATCCGAGGGCGCGATATCAGCCAGGCGACCTCTGGACCGCCCTGGCCCGG
CGACCCCGGATGGCACCCGATCGTGGGCCACCCGCTACCGCAACCTGTTCTCAATACCGGCCA
CGCACCCCTGGGTTGGACCATGGCTGCGGTCGGCTACCTGGCCGACCTGATGGCGAAGAAG
CGCCCGCAGATCAGTACCGAAGGCCGGATATTCCCGCTACAGCAATTCCCCGGAGAACGCCAAGA
ATGCCCATCCAGCGCACACTAA

```

The VIR4 protein (SEQ ID NO:8) encoded by SEQ ID NO:7 is presented using the one-letter amino acid code in Table 6B.

**Table 6B. Encoded VIR4 protein sequence (SEQ ID NO:8)**

```

MRVLVLGSGVIGTASAYYLARAGFEVVVVDRQDGPALETSFANAGQVSPGYASPWAAPGIPLKAM
KWLLEKHAPlAIKLTSDPSQYAWMLQMLRNCTAERYAVNKERMVLSEYSRDCLDELRAETGIA
EGRTLGTQFLRFTAQLDAAGKDIAVLERSGVPYEVLDRDGIARVEPALAKVADLKVGLRPLND
QTGDCQLFTTLaEMAKGLGVFRFGQNIERLD FAGDRINGVLVNGELLTADHYVLALGSYSPQL
LKPLGIKAPVYPLKGYSLTVPITNP EMAPTSTILDETYKVAITRFDQRIRVGGMAEIAGFDLSLN
P RRRETLEMITTDLYPEGGDISQATFWTGLRPATPDGTPIVGATTRYRNLFNTHGTLGWTMACG
SGRYLADLMAKKRPQISTEGLDISRYSNSPENAKNAHPAPAH

```

5

The role of VIR4 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

## MUT5

10       A *Pseudomonas* bacterial mutant (MUT5) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding imidazoleglycerol-phosphate synthase, cyclase subunit (hisF ; PA5140). This  
15       gene encodes the VIR5 nucleic acid (SEQ ID NO:9) shown in Table 7A.

**Table 7A. VIR5 Nucleotide Sequence (SEQ ID NO:9)**

```

ATGGCACTGGCAAAACGCATCATCCCCCTGCCCTGACGTGGACAACGGCCGAGTGGTCAAGGGCGTCA

```

```

AGTCGAGAACATCCGGACGCCGGCACCCTGCGAGATCGCTGCCGCTACGACGAGCAGGGTGC
CGACGAGATCACCTTCTCGATATCACCGCCAGCGTCGACGGCGGACACCACCCCTGCATACCGTC
GAGCGCATGGCTAGCCAGGTGTTCATCCGCTGACCGTGGCGGGCGTACCGCAGCGTGCAGGACA
TCCGCAACCTGTTGAATGCCGGCGGGACAAGGTCTCGATCAACACCGCCGGTGTCAACCCCGA
GTTCGTGGTGGAGGCCGGCACCCTCGGCTCGCAGTGCATCGTGGTGCCTCGACCGAAGAAG
GTTCCGCCCGGGCAGGCCGGCTGGAAATCTCACCCATGGCGGGCGCAAGCCCACCGGGC
TGGATGCCGCTCTGGCGAAGAAGATGGAAGACTTGGCGCTGGCAGATTCTCTGACCAGCAT
GGACCAAGGACGGCGTGAAGAGCGGTTACGACCTGGCGTGACCCCGCCATCAGCGAGGCGGTGAAC
GTGCCGGTGTACGCTTCCGGCGGTGGCAACCTGGAGCACCTGGCCCGGCATCTCGAGGGCA
AGGCCGACGCCGGCTCGCGGAGCATCTTCACTTCGGAGTACACCGTGCAGGAAGCCAAGGC
CTACCTGGCCAGCCGGTATCGTGGTGCCTGA

```

The VIR5 protein (SEQ ID NO:10) encoded by SEQ ID NO:9 is presented using the one-letter amino acid code in Table 7B.

**Table 7B. Encoded VIR5 protein sequence (SEQ ID NO:10)**

```

MALAKRIIPICLDVDNGRVVKGVKFENIRDAGDPVEIARRYDEQGADEITFLDITASVDGRDTTLH
TVERMASQVFIPLTVGGVRSVQDIRNLLNAGADKVSINTAAVNPVFVGEAADRFGSQCIVVAI
DAKKVSAPGEAPRWEIPTHGGRKPTGLDAVLWAKKMEDLGAGEIILLTSDQDGVKSGYDLGVTRA
ISEAVNVPVIASGGVGNLEHLAAGILEGKADAVLAASIFHFGETYVPEAKAYLASRGIVVR

```

5

## MUT6

A *Pseudomonas* bacterial mutant (MUT6) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding N-acetyl- $\alpha$ -glutamyl-phosphate reductase (ArgC; PA0662). This gene encodes the VIR6 nucleic acid (SEQ ID NO:11) shown in Table 8A.

**Table 8A. VIR6 Nucleotide Sequence (SEQ ID NO:11)**

```

ATGATCAAGGTGGCATCGTTGGCGGTACGGGTTATACGGGGTGGAACTGCTGCCCTGCTGGCGC
AGCATCCGAGGCCCGGGTGAAGTGTACACTCGCGTCCGAGGGGGGTGAAGGTGCCCGACAT
GTACCCGAACCTGCGAGGTCAATTATGACGACCTGCAGTTCAAGCGTGGCGACGCCAGCGCCTCGGC
GCCCGCACGTGGTGTCTCGCCACGCCGACGGCGTGGCGCACGCCGCTGGCTGGGAACGTGCTGG
ACGCCGGACCCGGTCATCGATCTGTCGCTGACTTCCGCTGGCGACGCCGAGGAGTGGCGCG
CTGGTACGCCAGCCGATGGCGTCCGGCGCTGCTCGACGAGGCTGTCTACGGCTGCCGAAGTG
AACCGCAGAGAATCCGCAGGCCGCTGATCGCCGTGCCGGCTGCTACCCGACCGCAGCCAGC
TGGGCTGATCCCGCTGCGAAGGCCGCTGCCGACGCCCTCGCGCTGATGCCGATTGCAAGTC
CGGGGTCAGCGGTGCGGGTGGCGGCCAAGGTTGGCTGCTGCTGCGAGGCCGGCGAAAGCATG
ATGGCCTACCGGGTCAAAGGGCATCGGCATCTCCGAAATCAGCCAGGGCTGCGTCCGGCTCCG
GCCGCAGCTGGCTGACGTTCTGACCGCACTGACGCCAATGATCCGCGGTATCCATGCAACCC
CTATGCCCATGTCGCGGATCGCTCGTCGACCTCCAGGGTTGTTGAGAAGCGCTACGCCGACGAA
CCCTCGTCGACGTGATGCCGGCGGCAGCCATCCGGAGACCCGCAGCGTGGCGCCAATGTCT
GCCGAATGCCGTGCATGCCCGGAGGCCGAGCTGGTGGTGGTGTGCGTGTGCGTGTGACAAACCT
GGTCAAGGGCGCCTCGGGTCAGGCCGCTCCAGAACATGAAACATCCTGTTGGCTGGACGCCGCTG
GGCCTCTCGCATGCCCTGCTCCCTGA

```

The VIR6 protein (SEQ ID NO:12) encoded by SEQ ID NO:11 is presented using the one-letter amino acid code in Table 8B.

**Table 8B. Encoded VIR6 protein sequence (SEQ ID NO:12)**

```
MIKVGIVGGTGYTGVELLRLLAQHPQARVEVITSRSEAGVKVADMYPNLRGHYDDLQFSVPDAQR
LGACDVVFATPHGVAHALAGELLDAGTRVIDLSADFRLADAEEWARWYQPHGAPALLDEAVYG
LPEVNREKIRQARLIAVPGCYPATQLGLIPLLEAGLADASRIIADCKSGVSGAGRGAKVGSFLFC
EAGESMMAYAVKGHRHLPEISQGLRRASGGDVGLTFVPHLTPMIRGIHATLYAHVADRSVLDQAL
FEKRYADEPFVDVMPAGSHPETRSVRGANVCRIAVHRPQGGDLVVVLVIDNLVKGASGQALQNM
NILFGLDERLGLSHAALLP
```

5 The role of VIR6 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

#### MUT7

10 A *Pseudomonas* bacterial mutant (MUT7) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydrolipoamide acetyltransferase (AceF; PA5016). This gene encodes the VIR7 nucleic acid (SEQ ID NO:13) is shown in Table 9A.

15

**Table 9A. VIR7 Nucleotide Sequence (SEQ ID NO:13)**

```
GTTGAGCGAACTCATTGCGTACCCGACATCGGCAACGGTGAGGGTGAAGTCATCGAGCTGCTGGTCA
AGCCCAGCGACAAGGTGAGGCCGATCAGAGCTGCTGACCCCTGGAATCCGACAAGGCCAGCATGGAA
AATCCCCAGTCCCAAGGCCGGGTAGTGAAAAGCATCAAGGCCGAAGGTCGGCGACACCTTGAAAGAA
GGTGACGAAATCTCGAGCTGGAAGTGGAAAGGCCGAACAGCCTGCCGAAGCCAAGGCCAGGCCAG
CGCCCGCCAACCGGAAGCGCGAAAGCCGAAGCGCCTGCTCCCGCCCCGAGCAGAGCAAGCCGGC
CGCCCCCGCCGCCAGCTCCAGGACATCAAGGTCCCGACATCGCTCGGCCGGCAAGGCCAAC
GTCATCGAAGTGTGGTCAAGGCCGGCACCGTCGAGGCCGACCGTGTGAGCTGATCACCTGGAAAT
CCGACAAGGCCAGCATGGAGATCCCTCGCCGGCCTCCGGGGTGGTGGAAAGCGTCTCGATCAAGGT
CGGTGACGAAAGTCGGCACCGCGACCTGATCTCAAGCTGAAGGTGGAAGGCCGCTCCGGCAGCC
GAAGAGCAACCGGCAGCCGCTCCGGCCAGGCCGCGCCGCCGAGCAGAAGGCCGCCGG
CGGCCCTGCCAGCCAAGGCCGATACCCGGCTCCGGTCGGCGACCCAGCCGACGGCGCAA
GGTCCACCCGCCGGGGGGGGGGCATGCTGGCGCGAGTTGGCTCGAGCTGAGCGAAGTGAAA
GCCAGCGTCCCAAGGGTGCATCTCAAGGAAGACGTCAGGTCTCGTCAAGGAGCAACTGCAGC
GCGCCAAGTCCCGCGGTGCCGGCGCCACCGGGAGGCCGATCCCGCCGATCCGGAAAGTCGACTT
CAGCAAGTTCGGCGAAGTGGAGAAAGTGGCATGACCCGGCTGATGCAAGGTGGCGCCGCAACCTG
CATCGCAGCTGGCTGAAGTGGCGACGTGACCGTACCTGAGCTGGACATCACCGACATGGAAG
CCTTCGGTGGCCAGAAGGCCGGGAGAAGGCCGGGTCAAGCTGACCGTACTGCCGATCCT
GCTCAAGGCCCTGCCACCTGCTCAAGGAACGTGCCGACTTCACAGTTCGCTGGCCCCCAGCGGC
AAGGCCGCTGATCCGCAAGAAGTACGTACACATCGGCTTCCGGCTGGACACTCCGGACGGCCTGCTGG
TCCCGGTGATCCGCGATGTCGACCGGAAGAGCCTCTGCAACTGGCCGGAGGCCGCCGACCTGGC
CGACAAGGCCGCAACAAGAAGCTCTGGCCGATGCCATGCAAGGGCCCTGCTCACCATCTCCAGT
CTCGGCCACATCGGCCGGCACCGGCTCACGCCGATGTCACGCCGAAAGTGGCGATCCTCGGTG
```

TGTCCAAGGGGACCATGCAGCCGGTATGGGACGGCAAGGCCTTCCAGCCGCCCTGATGCTGCCGCT GTCGCTGTCCTACGACCATCGCGTATCAACGGTGCCTGCCGCGCCTTCACCAAGGCCCTGGG GAGCTGCTGGCGACATCCGCACCCCTGCTCCTGTAA
--

The VIR7 protein (SEQ ID NO:14) encoded by SEQ ID NO:13 is presented using the one-letter amino acid code in Table 9B.

**Table 9B. Encoded VIR7 protein sequence (SEQ ID NO:14)**

MSELIRVPDIGNGEGEVIELLVKPGDKVEADQSLLTESDKASMEIPSPKAGVVKSIAKVGDTL KEGDEILELEVEGGEQPAEAKAAEAAAPAQPEAPKAEAAPAPAPSESKPAAPAAASVQDIKVPDIGSA GKANVIEWMVKAGDTVEADQSLLTESDKASMEIPSPASGVVESVSIKVGDEVGTGDLILKLKVE GAAPAAEEQPAAAPAQAAAPAAEQKPAAAAPAPAKADTPAPVGAPSRSRGAKVHAGPAVRMLAREF GVELSEVKASGPKGRIKEDVQVFVKEQLQRAKSGGAGATGGAGIPIPVEVDFSKFGVEEVAMT RLMQVGAANLHRSWLNVPHTQFDQSDITDMEAFRVAQKAAEAKGVKLTVPILLKACAHLLKE LPDFNSSLAPSGKALIRKKYVHIGFAVDTPDGLLVPVIRDVDRKSSLQLAAEAAADLADKARNKKL SADAMQGACFTISSLIGHIGGTGFTPIVNAPEVAILGVSKATMQPVWDGKAFQPRMLPLSLSYDH RVINGAAAARFTKRLGELLADIRTL
--

5

### MUT8

A *Pseudomonas* bacterial mutant (MUT8) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding NADH dehydrogenase I chain H (nuoH; PA2643). This gene encodes the VIR8 nucleic acid (SEQ ID NO:15) shown in Table 10A.

**Table 10A. VIR8 Nucleotide Sequence (SEQ ID NO:15)**

ATGAGTTGGCTGACTCCCGCTCTGGTCACCATCATCCTCACCGTGGTCAAGGCCATCGTGGTGTGCTGC TCGGCGTGGTCATCTGCGGCCCTGCTAACGCTGGTCAGCGCCGCTGCTGGCCCTGCGCAGGA CCGCTACGGCCCCAACCGGGTCGGTCCGGTGCCTTCCAGCTCGCGCGAACATGGTCAAGATG TTCTTCAAGGAGGACTGGACCCCGCGTTCGGCGACAAGATGATCTTACCCCTGGCCCCGGTAATCG CGATGGCGCCCTGCTCGCCTTCGCCATCGTGGCGATCACCCCCCACCTGGGGCGTGGCGGACCT GAACATCGGCATCCTGTTCTTCGCCATGGCGGCTGACGGTGTACGCCGTGCTGTTGCGCCGG TGGTCGAGCAACAACAAGTTGCCCTGCTCGGCAGCCTGCGCCCTCGGCCAGACCATTCCTACG AGGTGTTCTGGCCCTGCTGCTGATGGGATCGTCCGGCCAGGTGGCTCGTTCAACATGCGCGACAT CGTCCAGTACCAAGATCGACAACGTCGTTCATCATTCCGAGTTCTCGGTTCTGCACCTTCATC ATCGCCGGCTGCCCGTACCCACCGTCACCGGTTGACCGAGCCGGAAAGCGGAGCAGGAACCTGGCG ACGGCTACCAACATCGAGTACGCCGGGATGAAATGGGCATGTTCTTCGTCGGCGAGTACATCGGCAT CGTACTGGTCTCGCGCTGCTGGCGACCCCTGTTCTCGGCCGGCTGGCACGGTCCGTTCTGGACACC CTGCCCTGGCTGCTTCTACTTCGCGCCAAGACCGGCTTCTCATGCTCTTCATCCTGA TCCCGCCCTCGCTGCCCGCTCCGCGCTATGACCAAGGTGATGGCGTTAGCTGGAAAGGTGTGGCCTGCC GCTGACCCCTGATCAACCTGCTGGTACCGGGCGCTCGTGGCCGGCCAGTAA
--

The VIR8 protein (SEQ ID NO:16) encoded by SEQ ID NO:15 is presented using the one-letter amino acid code in Table 10B.

**Table 10B. Encoded VIR8 protein sequence (SEQ ID NO:16)**

```
MSWLTPALVTIILTVKAIIVVLLAVVICGALLSWVERRLLGLWQDRYGPNRVGPFGAFQLGADMVKMFFKEDWTPPFADKMIFTLAPVIAMGALLVAFAIVPITPTWGVADLNIGILFFFAMAGLTVYAVLFAGWSSNNKFALLGSSLRASAQTISYEVFLALSLMGIVAQVGSFNMRDIVQYQIDNVWFIIPQFFGFCTFIIAGVAVTHRHPFDQPEAEQELADGYHIEYAGMKWGMFFVGEYIGIVLVSALLLATLFFGWHGPFLDTLPWLSSFFYFAAKTGFIMLFILIRASLPRPRYDQVMAFSWKVCLPLTLINLLVTGALVLAQQ
```

## 5 MUT9

A *Pseudomonas* bacterial mutant (MUT9) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the 10 gene encoding pyoverdine synthase D (PvdD; PA2399). This gene encodes the VIR9 nucleic acid (SEQ ID NO:17) shown in Table 11A.

**Table 11A. VIR9 Nucleotide Sequence (SEQ ID NO:17)**

```
GTGCAAGCACTCATAGAGAAGGTGGGCTCCCTTCCCCCAGGAAAGGAAGGCATTGGCTGTCCTGC  
TCAAGCAGCAAGGTGTCATCTCTTCAGATCGGCCAGTGTCAAGCGCCAGGACGGCGAGCCCCCT  
GCGGCTCTCCTATGCCCAAGGAGCGACAGTGGTTCTCTGGCAACTGGAGGCCAAAGCGCGGCCCTAC  
CATATCCCGAGGTGTCCTGGCTTACGTGGGCGCTGGACCTGGATGCCCTGCAACGCAGCTTCGACA  
GCCTGGTTGCGCGGACGAGACCCCTACGCACCCGTTTTCGCCTCGACGGCGACGAGGCCAGGAG  
GATCGCCGCATCCATGGCATTGCCGTTGGATATCGTCGCGTTGGGGCCGCTCGAGGAGGGGCCCTC  
GCTCGGCAGGTGAGACGACGATCGCGGCCGTTGACTGGAGCGTGGGCCGCTGCTGCCGGTGA  
GCCTGTTGCCGGTGGCCAGGACGACCATGTCGTTGGTGTGGTCCAGCATTACATCGTGTCGACGG  
TTGGTCGATGCAAGGTGATGGTCGAGGAACAGTGGTCCAGCTATGCCCTATAGTCGAGGGCTCGAG  
GTAGCGCTGCCGGCTTGGCGATCCAGTACCGGACTACGCCCTGTCGAGGCCAGCTGGATGGAGG  
CCGGGGAAAAGGAGCGCCAGTTGGCGTACTGGACCGGCCCTGTCGGGGCCGAGCAGCCGGTCTGGA  
GTTGCCGTTGCAACGGGCCGCGCCGGTTGCGCAAAGCCATGTCGTTGGCCAGTTCATCCTGGAACGTG  
GATATTGATCTGCCCAGGCCTCACGGCGTGGCCCAGCAGGAGGGGGCTACTGCCCTGCCCTGT  
TGCTGGCTTCGTTCCAGGCCTGCTGTATCGCTACAGCGGGCAGGCCGATATCGTGTGCCGTGCC  
GATCGCAATCGCAACCGCGTGGAGACCGAGCGGCTGATCGGCTTCTCGTCAACACCCAGGTGCTC  
AAGGCCGACCTGGACGGTCGGATGGGCTTCGACGAGCTGCTGGCCCAGGCCCAACGCCGCGCTGG  
AGGCCCAAGGCCGACCGAGGACCTGCCGTTGAGCAACTGGTGGAGGCCCTGCAAGCCGGAGCGCAGTCT  
TAGGCCACAAACCGCTGTTCCAGGTGCTGTTCAACTACCAAGAGCGAAGGCCGTGCCAACGCCAGGCA  
TCCGCTTCGAGGACTACAGATGGAAGAGCGTGCAGTTCGACAGCGGCCAGGGCAGTTCGACTTGA  
CGTTGGACCTGACGGACGAAGAGCGCAGCGCTTGGCCGCTTTCGACTACGCCACCGACCTGTTGCA  
CGCCCTCACCGTGGAACGCCCTGCCGCTTGGCGCAACCTGTCGCGCCGAGCAGCCCAACCCCA  
CGACAGCGGCTCGCGAGGTGCGCTGCTGGATGCGCCGGAGCGCCGGCAGACCCCTCTCCGAATGGA  
ACCCGGCCCAGCGCAGTGCCTGGCAGGGCACCTTGCAAGCAGCGTTGAGGAACAGGCCGGCA  
ACGGCCACAGGGCGTTGCGCTGATCCTCGACGAACACGGTTGAGCTACGGCAACTGAATGCCG  
GCCAATCGCCTGGCGCACTGCCTGATGCCCTGGCGTTGGCGCGACGTGCCGGTGGCGC  
TGGAGCGTTGCGCTGGACATGCTGGCTGGCTGCTGGCGATCCTCAAGGCCGGGCCACCTG  
GTTGGACCCGGCGGCCAGAGGAGCGCCTGGCGCATATCTCGACGACAGTGGGGTACGGCTGCTG  
CTGACCCAGGGCATCTGCTCGAGCGCCTGCCACGGCAGCGGGGGTGGAGGTGCTGCCATCGACG  
GACTGGTGCTGGACGGCTACGCCAGAGCGATCCGCTCCGACGCTATCGCGGACAACCTGGCCTA
```



```

AACGGGTGGCCTGGACGACAACCTCTCGAACTGGGGGGTCACTCATTGTTGCTGCTGATGCTCAA
GGACGGATCGCGATACCTGCCAGGCTACGCTGAGCAGCCAACTGATGACCCATGCCAGCGTC
GCGAACAGGGGGCATCGAGGGCAGGGCGGTGAGTCGTTGCTGGTGCCTCAACGGCAGGC
GCGAAGGTTCCGCCGCTTCAATGTTCCATCCGAGTTGGCTCTGTCAGTGTACAAGACCCCTCGC
CATGGCCTGCCGGATCGTCATCCGGTCAAGGGTGTGCTGCCGTGCCCTGCTGGCGCTGGTCGC
GAGGTGCCGGAGTGGGACGATATGGTTGCCGAAATGCCGAGCAATTGCTGCAGGAGCACCCCGAAG
GGGTTTCAACCTGCCGGATGGTCGCTGCCGCAACCTGCCGATGGATGTCGCCGGCCGGCTGGA
GCAGCGTGGGCCGAGGGCTTCGCGCTGGATCGACCGCCGACCGGTCAGGGTCAGGGTCAGCG
TTCTGGAACGAGATCGGGCCGACGCCGGAGGCAGTCCGAACCTATCCGTGGCGAGATGCGGGTGG
AACTGCTCGGTGTCATGTTCCGGAGCGGGCCGAGCATACTGAACGGGCTGGCATCGATCTGCTC
CGCCACGACGGACGATGAGCAGCGCTGGACGAGGATGAGCAGACTGGCGGAAGGGAGATGGCGCC
GAGTCGCGACACTGCCAGCGAAATGCCAGAGCAACGAACACTGGAAGTGTCTGGGAGTTGAAAC
AGATCCTCGACGAGCGCTGAAAGCGATGGATTACCCGGTCTGACGGCGAAGGTGAGCTCTGGT
GGCCGCGCGCAGCACCAATGCCATCCAGCGGAGCGCGGTGGAGCGCTGATGCCGAGGGGATCGG
GCTGAGCGTGTGCAACCGGTGCGGGTGTGATACCCGGCACGACAAGATCATCGACCACCTGAGT
TTGTGCAGAGCTTCCGGGCCCTGGAGCGTGCCTGGCGCTGA

```

The VIR9 protein (SEQ ID NO:18) encoded by SEQ ID NO:17 is presented using the one-letter amino acid code in Table 11B.

**Table 11B. Encoded VIR9 protein sequence (SEQ ID NO:18)**

```

MQALIEKVGSLSQERKALAVLKLQQGVNLFEIAPVFKRQDGEPLRLSYAQRQWFLWQLEPESA
AYHIPSVLRLRGRLLDALQRSFDSLVARHETLRTFRFLDGDEARQEIAASMALPLDIVALGPLE
EGALARQVETTIARPFDLERGPLLRSVSLRLAEDDHVLVLVQHIVSDGWSMQMVEELVQLYAA
YSRGLEVALPALPIQYADYALWQRWSWMEAGEKERQLAYWTGLLGEQPVLPLFDRPRPVRQSHR
GAQFILELDIDLSQLRRAVQQEGATAFALLASFQALLYRYSSQADIRVGVPIANRNRVETERL
IGFFVNTQVLKADLDGRMGFDELLAQRQRALEAQAHQDLPFEQLVEALQPERSLSHNPLFQVLF
NYQSEARGNGQAQFRFDELQMESVQFDSRTAQFDLTLDTDEEQRFCAVFDYATDLFDASTVERLA
GHWRNLLRGIVANPRQRLGELPLLDAPEPRTQTLSEWNPAQRECAVQGTLQQRFEEQARQRPQAVA
LILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLDMVLGLLAIIKAGGAYLPLDPA
APEERLAHILDDSGVRLLLTOGHLLERLPRQAGVEVLAIDGLVLDGYAESDPLPTLSADNLAVI
YTSGSTGPKGTLLTHRNALRLFSATEAWFGFDERDVWTLFHSYAFDSVWEIFGALLYGGCLVI
VPOWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACSADMATQQPALRYVIFGGEALDLQSL
RPWFQRFQDRQDQPLVNMGYITEETTVHVTYRPVSEADLEGGLVSPIGGTIPDLSWYILDRLDNPVP
RGAVGELYIGRAGLARGYLRRPGLSATRFPVPNPFPGGAGERLYRTGDLARFQADGNIEYIGRIDH
QVKVRGFRIELGEIEAALAGLAVRDAVVLAHGVGGTQLVGYYVADSAEDAERLRESLRESLKR
HLPDYMVP AHLMLLERMPLTVNGKLDQALPQPDASLSQQAYRAPGSELEQRRIAIIWSEILGVER
VGLDDNFFELGGHSLLATRVISRVQEQQLDASLKFALFERPVLLEFAQGLERTTDAVSTIPLADR
QOPLALSFAQERQWFLWQLEPESAAHYIPSALRLRGRLDVDALQRSFDLSVARHETLRTFRFLEG
GRSYQQVQPAVSVSIEREQFGEELTIERIQAIVVQFDLERGPPLRVNLLQLAEDDHVLVLVQHH
IVSDGWSMQMVEELVQLYAAYSQGLDVLPALPIQYADYALWQRWSWMEAGEKERQLAYWTGLLG
GEQPVLELPFDRPRPARQSHRGAGQLGFELSRELVEAVRALAQREGASSFMLLLASFQALLYRYSG
QADIRVGVPIANRNRVETERLIGFFVNTQVLKADLDGRMGFDELLAQRQRALEAQAHQDLPFEQ
LVEALQPERNASHNPLFQVLFNHQSEIRSVPVQLEDLRLEGLAWDGQTAQFDLTLDIQEDENG
IWASFDYATDLFDASTVERLAGHWRNLLRGIVANPRQRLGELPLLDAPEPRTQTLSEWNPAQRECA
VQGTLQQRFEEQARQRPQAVALILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLD
MLVGLLAIKAGGAYLPLDPAPEERLAHILDDSGVRLLLTOGHLLERLPRQAGVEVLAIDGLVL
DGYAESDPLPTLSADNLAYVIYTSGSTGPKGTLLTHRNALRLFSATEAWFGFDERDVWTLFHSY
AFDFSVWEIFGALLYGGRLVIVPQWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACSADMA
TQQPALRYVIFGGEALDLQSLRPWFQRFQDQPLVNMGYITEETTVHVTYRPVSEADLKGGLVSP
IGGTIPDLSWYILDRLDNPVPRAVGELYIGRAGLARGYLRRPGLSATRFPVPNPFPGGAGERLYR
TGDLARFQADGNIEYIGRIDHQVKVRGFRIELGEIEAALAGLAVRDAVVLAHGVGGTQLVGYV
VADSAEDAERLRESLRESLKRHLPDYMVP AHLMLLERMPLTVNGKLDQALPQPDASLSQQAYRA
PGSELEQRRIAIIWAEILGVERVGLDDNFFELGGHSLLLMLKERIGDTCQATLSISQLMTHASVA
EQAACIEGQARESLLVPLNGRREGSPLFMFHPSPGSVHCYKTLAMALRDRHPVKGVVCRALLGAG
REVPEWDDMVAEYAEQLLQEHPEGVFNLAGWSLGGNLAMDVAARLEQRGRQVAFVGWIDAPAPVR
VEAFWNEIGPTPEAVPNLSVGEMRVELLGVMFPERAEHIERAWSSICSATTDDEQRWTRMSDWAE
AEIGAEFATLRSEIAQSNELEVSWELKQILDERLKAMDYPRLTAKVSLWWAARSTNAIQRSAVER
SMAEAIGAERVEPVRLDTRHDKIIDHPEFVQSFRAALERAGR

```

## MUT10

A *Pseudomonas* bacterial mutant (MUT10) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the RND multidrug efflux transporter MexD (mexD; PA4598). This gene encodes the VIR10 nucleic acid (SEQ ID NO:19) shown in Table 12A.

**Table 12A. VIR10 Nucleotide Sequence (SEQ ID NO:19)**

```

ATGTCCGAATTCTCATCAAGCGGCCGAACTCGCCTGGTGGTGGCCCTGTTCATCTCCCTGGCCG
GCCTGCTGGTCATTTCAAATTGCCGGTAGCGCAGTACCCCAATGTCGCGCCGCCACAGATCACCAT
CACCGCACCATATCCCGCGCCTCGCGAAGGTGCTGGTGGACTCCGTCACCAGTGTGCTCGAGGAG
TCGCTGAACGGCGCCAAGGGCCTGCTACTTCGAGTCGACCAACAACCTCAAACGGCACCGCCGAGA
TCGCTGTCACCTTCGAGGCCGGCACCGATCCGGACCTGGCCCAGGTGGACGTGCAGAACCGCCTGAA
GAAAGCCGAGGCCGGCATGCCGAGGCCGGTGTGACCCAGGGCCTGAGGTGAGCAGACCGAGCGCC
GGTTCTCTGCTGATCTATGCGCTCAGCTACAAGGAAGGGCGCTCAGCGCAGCGACACCACCGCCCTCG
GCGACTACGCCCGCGCAATATCAACAAACGAGCTCGGGCGCTGCGGGCGTCGGCAAGCTGCAATT
CTTCTCTCCGAGGCCGGCATGCGGTCTGGATCGATCCGAGAACAGTGGTGGGCTCGGCCTCTCC
ATCGACGACGTGAGCAATGCCATCCGGGGCAGAACGTCAGGTGCGCCGGCGCCTCGGCAGCG
CACCGGGCAGTCCCGCGCAGGAGCTGACGGGACCCCTGGCGGTGAAGGGCACCTGGACGATCCGCA
GGAGTTCGGCCAGGTAGTAGTGTGCGCGCCAACGAGGACGGCTCGCTGGTCCGGCTCGCGATGTCGCG
CGCCTGGAACTCGGCAAGGAGAGCTACAACATTCTCGCAGCTGAAACGGCACGCCACCGTGGGCG
GGCTATCCAGCTGTCGCCGGGGCAACCGCATCCAGACCGCTACCCCTGGTAAACAGCGTCTCGC
CGAACCTGTCGCCGTTCTCCCGAGGACATGAGTACAGCGTGCCTACGACACCTCGCCTTCGTC
GACGTGGCCATCGAGAAAGGTGATCCACACCCCTGATCGAAGCGATGGTCTGGTGTTCCTGGTGTGATGT
TCCCTGTCCTGAGAACAGTCCCTACACCCCTGATCCCGCATCGTGGTGCCTGGTGTGCTGCTGGG
TACGCTGATGGTGTGATGTAACCTGCTGGGTTCTCGGTGAACATGATGACCATGTTCGGCATGGTCTG
GCGATGGCATCTGGTGGACGACGGCATCGTGGTGGAGAACGTCAGCGGATCATGGCGGAGG
AGGGGATTTCCCGGCCAGGCCACGGTCAAGGGCATGAAGCAGGTATCCGGCGCATCGTCGGCAT
CACCTGGTGTCTCGGGGTGTTCTGCCGTGGCTTCATGCCGGTTCGGTGGGGTGATCTAC
CAGCAGTTCTCGGTGTCGCTGGCGTCTCGATCCCTGTTCTCCGGCTTCTCGGCCCTGACCTTCACCC
CGCGCTGTGCCACGCTGCTCAAGCCATTCCGAAGGGCACCGAGAACGCGGGCTTCGG
CGCTTCAACCGTGGCTCGCCCGCGTACCGAGCGCTATTGCTGCTCAACTCGAAGCTGGTGGCG
CGGCCGGACGCTTCATGCTGGTGACGCCGCTGGTGGCATGCTGGCTACTTCTACCTGCGCC
TGCGGAAGCCTCGTGCCGGGAAGACCTCGGCTACATGGTGGTCACGTGCAACTGCCGCTGG
CGCTTCCGGCGTGGCAGCGATGCCACCGGGCAGGAGCTCGAGCGCTTCTCAAGTCCCCGAGGCG
GTGGCTTGGTGTGTTCTGATCTGGGTTCTCAGCTTCTCCGGCCAGGGCGACAATGCCGCGCTGGCCT
TCCAACCTTCAAGGACTGGTCCGAGCGAGGCCGAGCAGTCGGCCGCCGAGATGCCGCGCT
GAACGAGCATTTCGCGTCCCGACGATGCCACGGTCACTGGCGTGTGCGGCCACCGATCAACGGT
CTGGTAACCTCGCGGTTCGCATTGCCCTGATGGACCGTAGGGGGTGGCGCGAAGCGCTGC
TGCAGGCTCGCGATACTCTTCTTGGCAGATCCAGCAACCCGAATTCTTACGCGATGATGGA
AGGACTGGCGAAGGCCGCAACTCGCCGCTGTTGATCGACGGGAGAACGGGGTGGCCCTGGGGTG
AGCTTCGAGACCATCAGCGGACCGCTGTCGCTGCCCTGGCTCGGAGGTGATCAACGACTTCACCA
ATGCGGGGCCAACAGGGTGGTGTATCCAGGCCAACAGGGCAACCGGATGACCCCGAAAGCGT
GCTCGAGCTATACGTCCTAACGCTGCTGGCAACCTGGTACCGCTCAGCGCCTCGTCAGCGTAAA
TGGGAAGAGGGACCGGTGCAATTGGTGGCCTATAACGGCTACCGCTGATCCGCATGTCGGTGACG
CCGGCCCGGCTTCAGTACCGCGAACGCCATGGCGAAATGGAGGCCCTGGCTCGCAGCTGCCGGC
CGGCATCGGCTACGAGTGGACCGGGCTGTCCTATCAGGAGAACGGTCTCCGCCGGGAGGCCACCGC
CTGTTGCCCTGCCATCTGGTGGTGTCTGGCTCGGCGCTACAGAGAGCTGGTCGATCC
CGCTGCGGTGATGCTGATCGTGGCGCATGGCGCCTGCGCGGTGATGGTCAGCGGG
TATGTCCAACCGACGTGTATTTCAGGTCGGCCTGATCACCATCATCGGTCTTCGGCGAAGAACGCG
ATCCTCATCGTCGAGTTGCCAAGGAACCTCTGGAGCAGGGGATAGCCTGCCGACGCCGCCATCG
AGGCCGCCGCGCTGCCCTCCGGCCGATCATGACTTCCATGGCGTTCATCCCTGGCGTGAATACC
CCTGGCCCTGGCCAGCGGTGCCGGCGGGCAGGCCAGCGTGGCCATGGCACCAGGAGTGTGATGGGG
ATGCTCAGGCCACCTCCTCGCGTGTGCTGTTGACCTATCTGTTGCTGGCTGCTGCGCTG

```

TGCGCAGCAAGCCGGCACCCATCGAACAGGCCGTTGCCGGGGAGTGA

The VIR10 protein (SEQ ID NO:20) encoded by SEQ ID NO:19 is presented using the one-letter amino acid code in Table 12B.

**Table 12B. Encoded VIR10 protein sequence (SEQ ID NO:20)**

MSEFFIKRPNFAWVVALFISLAGLLVISKL PVAQYPNVAPPQTITATYPGASAKVLVDSVTSQL  
 EESLNGAKGLLYFESTNNNSNGTAEIVVTFEPGTDPLAQVDVQNRKKAEARMPQAVLTQGLQVE  
 QTSAGFLLIYALSYKEGAQRSDTTALGDYAAARNINNELRRLPGVKLQFFSSEAAMRVWIDPQKL  
 VGFGLSIDDVSNAIRQNVQVPAGAFGSAPGSSAQELTATLAVKGTLDDPQEFGQVVLRANEDGS  
 LVRLADVARLELGKESYNISSSRLNGTPTVGGAIQLSPGAGNAIQTATLVKQRLAELSAFFPEDMQY  
 SVPYDTSRFVDAIEKVIHTLIEAMVLVFLVMFLFLQNVRYTLIPSIVVPCVLLGTLVMYLLGF  
 SVNMMTMFGMVLAILVDDAIIVVVENVERIMAEEGISPAAETVKAMKQVSGAIVGITALVLSAVF  
 LPLAFMAGSAGVVIYQQFSVSLAVSILFSGFLALTFTPALCATLLKPIPEGHHEKRGFFGAFNRGF  
 ARVTERYSSLNSKLVARAGRFMLVYAGLVAMLGYFYRLPEAFVPAEDLGYMVVDVQLPPGASRV  
 RTDATGEELERFLKSREAVASVFLISGFSGQCDNAALAFPTFKDWSERGAEQSAAEIAALNE  
 HFALPDDGTVMAVSPPPINGLGNSSGGFALARLMRSGVGREALLQARDTLLGEIQTNPKFLYAMME  
 GLAEAPQLRLIDREKARALGVSFETISGTLSAAFGEVINDFTNAGRQQRVVIQAEQGNRMTPE  
 SVLELYVPNAAGNLVPLSAFVSVKWEEGPVQLVRYNGPSIRIVGDAAPGSTGEAMAEMERLAS  
 QLPAGIGYEWTGLSYQEKSAGQATSLFALAILVVFLLVALYESWSIPLSVMLIVPIGAIGAVL  
 AVMVSGMSNDVYFKVGLITIIGLSAKNAILIVEFAKELWEQGHSLRDAIAEAARLRFRIIMTS  
 AFILGVIPLALASAGAGAASQRAIGTGVIGGMLSATFLGVLFVPICFVWLLSLRSKPAPIEQAA  
 AGE

5

## MUT11

A *Pseudomonas* bacterial mutant (MUT11) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA3721. This gene encodes the VIR11 nucleic acid (SEQ ID NO:21) shown in Table 13A.

**Table 13A. VIR11 Nucleotide Sequence (SEQ ID NO:21)**

ATGAACGATGCTTCTCCCCGTCGACCGAACGCCGAGGCAACGCCGCCATGCTGACGCCG  
 CTACCCAGGCCTTCTCGAACACGGTTTCGAAGGCACCACCCCTGGACATGGTGATAGAACGGCCGG  
 TGGTTCACGGGGACCCCTGTACAGCTCCTCGCGCGAAGGAGGGCTGTTGCCGCCGATCGCC  
 CACATGATCGGGAAATCTCGACGACAGCGCCGATCAGCCGCCGCCACGCTGAGCGCCA  
 CCCTCGAGCATTCGGCCGGCGTTCTCACCAAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCG  
 CCTGGTGGTGGCGGAATCCCCGCGGTTCCGGCGATCGGCAAGTCCCTACAGAGCAGGGCCGAG  
 CAGAGCTATCTGCTGCTCAGCGAGCGACTGGCCGGCTGCTCCTCACATGGACGAGGAAACGCTCT  
 ACGGCGTGGCTGCCAGTTCTCGAGATGCTCAAGGCCACCTGTTCCCTCAAGGCCCTCAGCGTGGC  
 CGACTTCCAGCCGACCATGGCGCTGCTGGAAACCCGCCCTCAAGCTGCGTGGACATCATGCCCTGC  
 TACCTGGAACACCTGTCGAGAGCCCCGCGCAGGGCTGA

The VIR11 protein (SEQ ID NO:22) encoded by SEQ ID NO:21 is presented using the one-letter amino acid code in Table 13B.

**Table 13B. Encoded VIR11 protein sequence (SEQ ID NO:22)**

```
MNDASPRLTERGRQRRAMLDAATQAFLEHGPEGTTLDMVIERAGGSRGTLYSSFGGKEGLFAAV
IAHMIGEIFFDSADQPRPAATLSATLEHFGRRLTSSLDPRCQSLYRLVVAESPRFPAIGKSFYE
QGPQQSYLLLSERLAAVAPHMDEETLYAVACQFLEMLKADLFLKALSVADFQPTMALLETRLKLS
VDIIACYLEHLSQSPAQG
```

## 5 MUT12

A *Pseudomonas* bacterial mutant (MUT12) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the 10 gene encoding PA0596. This gene encodes the VIR12 nucleic acid (SEQ ID NO:23) shown in Table 14A.

**Table 14A. VIR12 Nucleotide Sequence (SEQ ID NO:23)**

```
ATGTCTGATGATGCCCGTTCCAGCAGCTGAATTGCTGGTTGGACTCTTGTGCCCCGAGTTGTTCG
TTGCCGAAGGTTGGGGGAAGTGCCTCCCCGCCGAACTGATCCCGGCCAGTAGCGACGCCAGCTTCCG
TCGTTATTCCCGTGGCAGGGAGGGGACCGCAGCCTGGTGGTGTGGACGCGCCGCCGCCAGGAA
GACTGCCGACCGGTTCTGTCAGGTCGGCCGGACTGCTCGCCGGAGCCGGCGTGCATGTGCCGAGGATTC
TCGCCCAGGACCTGGAGAACGGTTCTCTGCTGTCAGTGACCTGGGCCGGCAGACCTACCTCGACGT
GCTTCATCCCGGAATGCCGACGAGCTGTTCTGCAACCGGGCTGGATGCGCTGATCGCCTTCCAGAAG
GTCGATGTCGCCGGTGTCCCTGCCCTGCCCTACGACGAAGCGCTGCTGCCGGAGCTGCAGCTGTTCC
CCGACTGGTACCTGGCCGCCACCTCGGCGTGGAGCTGGAGGGCGAGACGCTGGCCCGCTGGAAACG
GATCTGCGACCTGCTGGTACGCGAGCGCTGGAGCAACCCGGGGTCTCTGACTTCCAGGACGCCCTGCACGGCC
CCCGCAATCTGATGCTCAGCGAGCCCAACCCGGGGTCTCTGACTTCCAGGACGCCCTGCACGGCC
CGGTACCTACGATGTCACCTGCCCTGTACAAGGACGCCCTCGCAGTTGGCCGGAGCCGGCGTGC
TGCCCGCGTGAACCGTTACTGGAGAACGGCAGCTGGCCGGCATCCCGTGCAGGCCAACGTTCGAA
GACTCCCTCCGCGCCAGCGACCTGATGGCGTGCAGCGCCACCTGAAGGTGATGGCATCTCGCCC
GTATCTGTCACCGCGACGCCAACGGCGCTACTGGGTGACGTGCCCGCTTCCGTTATCTGGA
AACCGCCGTGGCGCCGCTCCGAGCTGGCCGAACTGGCGAGCTGCTGGCCTCGCTGCCGCAGGGA
GCCGAGGCATGA
```

The VIR12 protein (SEQ ID NO:24) encoded by SEQ ID NO:23 is presented using 15 the one-letter amino acid code in Table 14B.

**Table 14B. Encoded VIR12 protein sequence (SEQ ID NO:24)**

```
MSDDARFQQLNWLDSCLPELFVAEGWGEVPPAELIPASSDASFRRYFRWQGGDRSLVVMMDAPPP
QEDCRPFVKVAGLLAGAGVHVPRILAQDLENGFLLSDLGRQTYLDVLHPGNADELFEPALDALI
AFQKVVDVAGVLPAYDEAVLRELQLFPDWYLARHLGVELEGETLARWKRICDLLVRSALEQPRVF
VHRDYMPPRNLMLEPNPGVLDQDALHGPVTDYDVTCLYKDAFVSWPEPRVHAALNRYWKKATWAG
```

IPLPPSFEDFLRASDLMGVQRHLKVIGIFARICH RDGKPRYLG D VPRFF RYLETAVARRPELAE GELLASLPQGAEA
---

### MUT13

A *Pseudomonas* bacterial mutant (MUT13) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA5265. This gene encodes the VIR13 nucleic acid (SEQ ID NO:25) shown in Table 15A.

**Table 15A. VIR13 Nucleotide Sequence (SEQ ID NO:25)**

ATGAGCGGATCCAGGACCAGAGTATCGACGAAGGCGTGC CAAGCGCACCGCCTACCA GAAACGATC GGCGTGCACGACTGGCATTGAAACGTCGAGCGACAGGACGGCGGTATCCCTGCAGATTCGGTGGCCAG CGATATGCTCGGCCATGAGGAGCAGCGCTATCCAGCAGAACACCTTCCTGGCTGTGATGCCGCTG GTCGCCTGCCAACGCTGGCAAGGCCGGTTATGGCAGCAGCTGCCGCCGGCGCCTACCGCGGG CGGGACGGATCTACCTGTTCCAGGACGGCAAGTTGTGGCGCAACTGGAATGTGATGGCAAGGGCAA CCTGTTGAAAGTCGATCCTGCAGGGGCGCAGCCAGCGTGC GGACAAGCGTCCGGCTTAGGCAAG ACACAAGCGCTGATCCTGGTGGCGTGTGGCAAGGGCAGTTCGTGATCCCACGCTACACCATGG CCTATAGCGAAACTCCCTGGCCTTGGTGTGTAATCGACTGGCTGGAGGAGGACCCGCAAGCGGCTCAA CCGGCGCTGCCAGCAGATGGCGTCCCTGGAAACGCCCTGGTGGCAACCAGCACTGGAAAGCCTCC ATCCATCAACCCGCGCTGGTCATTGATCATCAGCGCCAGGGTTGGGACCTCGCAGCTCAACGTCG AGAGCGCGCTGGAAGACCCGGCGGAATTCAACACTGAGTTGCGCCCTTTCGCGAAGAGTCGCTGGT GTGCCAGTTGCAAGCAGCCAGCAGGAATTGGCGCCCTGCTGAAGCAGGCTCCGGCCCTCTGCGCTA CCTACTCTGGAAGCCGGAGAGGAGCTACTGGAAACCCCTCAAGCTGGTGGGCAATCCCAACCTCATCG GGCTGATGTCGACGACTCGCTGTCGCCCTGGCACCAGCTGCGGCCAGGCGCCACTGCGCCGC CTACTTGCGCAGCCTCAATGCACTGCTGCCGACCGTCCCAACGGAGCAGCTATGCACAGGTGCTGAGC AACATGTCGACGGCCCGCTCGCCAAGCTCAGGGCGAGGTGATCAGGCCGAACGGACAGGCGA TCTCGCCGAGGGAGCGACAGTCTGCGAATCCACCTGACGCAAGGTCGAGCATCTGGTTGCCCT GCTGGAAGGCCCTTGCACCCGGTTGCAAGGACTGGACCCACCAGTGCACGAAGCCCTGCTGGAG CCCTACAGCCTGATGAGCGAGGCACTGGCTGCCCTGAACCAGCTCCCGACCAGCTGCACGCACTGT ACAGCGGTACCGCCTACCGGGCGCTGGCGCACATGTCGAGCGGGTGGTCAGCACGGTTCTGCAGGC AAGCCACCGCTTGGGCCATGCTCTGGCCAAGGAGCAAGGACAACCTCCGAGCCGGTTCGGCGC CTGCAAGCGCTGCGGATAGCCCGGGACGCCGGACCCCGATGCAATGGGCTCAGCACGCTGATGC TGGGAGCCAGTCTGCTGGCGAGGTGACCGAGCCCAGCGCCGGAAAGAGCTCGCCTACTTCCCTGG CGACCTGCTGGACGTGTTGCGCCAGCGTAGTCGAGCAACTCGGCCGGCTGCTCCAGGGCGCCACC CAGATCCAGCTGACCGCTTGTCCACCGACCTTCAATACTCTGAGCGCCCTCTGGTGAAGATGA AAGGTATCCGCTGCTGCCGACAGTCAGGTGCCGCTGACATGGTTGTCGTCGGCGTGGCGGAGC CGGCGCTGCCAACGGTCTGACCGAGGTGAGGCCAGGAGCTGAGGCCAAGAGCTATGGCGCGCC ATCGTTCAAGGACGGTGCCTGGCAATCCCTGGCCGGCACCAGTCCCCCGACACCGGCATGAGTCGCG CCAACCTGCGCAACGTCATGGGGTGGCGTACCCAAAGGATCACCCGGACCTGCTTGCCTACACGAA ATTCCGTACGAGTTAGGCACGTTGACCCAGGTGATGGAGAACACTCGCAGTCGACGATGATG CTGGGTTTGCAGTTATAACTGAGTGCAGGTGCAAGGCATACAGTGGCTTGAGACAGTGGAG AAAAGCACAGAGGGACGATGGGGCTGCGTCAAGTGAATTCAGTAAACAGCGCTGGAGGAAGCCA TGCAAAGCTGCTTTCGGACCATCTACTGCAAAGTATCTAGAAACCCCAGTATATCGGTAGCCCAA ATATCCCCTCGATGGGCCAGGAATCTAGAAGTCAAACAGGCAGCCCTAAGTTAGGGTTGCTACGTG GGCTGGTGGCGCAGCCACACTATTGGTGCAGGCATCACTGTTGAGTGGGCTACCGAGCTTGGAG GCAGGGAGATAGCGATGCCGCTGCCGCTACGGTGTGGCCGAGTGGGTGGGGCCTTGGGGTGC TACGTCCTAGGATGGATAGTAAACCTTATGCTTTGCTGGCTGGTGGCGTTTGGCGATCGGAGGCA CTGTCGCTGCTAATCTACTGACTGACAGCGATGCCAAGGACCATCGTAAAGAAAGGCCCTCGGCCG GCAATTGCCGAGGCTGGCTGCTGCAATTGCGTGGAGTCCTCGGCCATCCGGGCTTTGTCCATGCC GACCCGAAACGGCTATGCCAATGCTGGAGTCCTCGGCCATCCGGGCTTTGTCCATGCC TGGAGAGCTGGCGCAAATTGGCGCCGGCGCAGTCGATCTGCTTGCAGGAAGCGGAACGGGTGCG CCAAGCGGTAGCCGACTGCGTATCCCTGCATCGACCCCAAGTTGCAAGGCGCTGGAGGCAAACGAT
---

TGGGCCGTGGTGCAGTTCCCGCTCCTGGCCATGTCGAGAATGGCCAGAAGGCGTCCGCCCTGG  
 TGGCCAGGAGTTCTCAGCAGCTGCCGATCGATCCGGCACCCCTGTCGGCTCAAGCGCTACCA  
 TCGGTCCCCCGGGCCAGCAGCTCGAAGCCTGCCGTTGGATGCTGCCAGCGCTATGTG  
 CTGCCGGCCAGCCTGCCGATTCCGAGTTGCTCCTCGGGCCGCTATAGCATGCGCATGACCCAGG  
 GTTGAAGATCAGCGCACAGTCGAACATGCCGACCAGCCTGAGCAGCGCTTGTCTGCCCTCA  
 ACCCAGCCCCGAAGAGTTGGAGTGCAATTACATCCGCCAATCGGTACCTCCCCGGACGACTGGGC  
 CCCCATGCTGCCACCTTATTGGTTGATAGAGAACAGTGAGTTAACGTATGA

The VIR13 protein (SEQ ID NO:26) encoded by SEQ ID NO:25 is presented using the one-letter amino acid code in Table 15B.

**Table 15B. Encoded VIR13 protein sequence (SEQ ID NO:26)**

MSGFQDQSIDEGVRKRTAYQNDRRARLALNVERQDGILQIPVASDMLGHEEHERIQQNTFLAVM  
 PLVRLPTLKGAGYGDQLPAGALPRAGRIYLFDQDGKLWRELECDGKGNLFEVDLLQGRSQRADKRP  
 ALGKTQALILVPVLVKQFVIPRYTMAYSETPWPWSYIDWLEEDPQRVNRCQQMASAWNANVAN  
 QHVKASIHQPLALVIDDHQAQGLRPRDFNVESALEDPAEFTPEFAAFREESLVCQLQRQQELAPLL  
 KQAPPSALPTLEAGEDVLETLKLRLRGPNLIGMLDDDSLFAIRHAAQARHCAAYLRSLNALLPHR  
 PNRGTYAQVLSNMLDGPLAKLRGEVDQAELEIFAEERQSCRILTQQVHEVLVALLEGPLHPVLO  
 DWTHQCDEALLEPYLSMSEALALNQLPDRCDALYSGTAYRALAAHVERVUSTVLQASHPLGAML  
 LAKDEGQLPEPVRRQLQALRDSPTPDAMGLSTLMLGASLLGEVDQPSAGKSLAYFLGDLDDV  
 GASVVEQLGRLSQGATOIQLDRLFAPTFNTLSALSVMKGIRLLPDSQVPLDMVVVGVRGAGLRN  
 GLTEVERQELRRKSYRRAIVQDGAGNPLAGTSPRDTGMSRANLRNVVAVPKDHPDLLAYTKFR  
 TQLGTLTQVMENTRIVPTMMLGFAIYNLNQVQAYSGFVDSGEKHRGTIGAVGAVIDLTAAGGSH  
 AKLLFGPSTAKYLETPRISVAQISPRWARNLEVQTGSPKLGLLRLGGAATLFGAGISVWDGYRA  
 LRQGDSDAAAAYGVAAVGGGLWGAYVLGWIVNPYALLAGAVLAIGGTVANLLTDSDAETIVKKG  
 PFGRQFAEAGLDSLMQDQRFIAHLKDPQTAYRQLLGVLGHPRVFRLEDWRKLAPAHRSVLO  
 EAERGRQAVSRTALSCIDPKLQALEANDWAVLSSPLLAMFENGQKAFLRVAQEFLSLPIDPGT  
 LFGVKRYHRVPAGPAKLEALPLDAASVLYLPASLPIPQLSPRARYSMRMTQGLKISAQFELNAD  
 QPEQLVLPQPSPKSWSAFTSANRYLPPDDLGPphaappywliensefnv

5

#### MUT14

A *Pseudomonas* bacterial mutant (MUT14) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin biosynthetic protein pchC (PA4229). This gene encodes the VIR14 nucleic acid (SEQ ID NO:27) shown in Table 16A.

**Table 16A. VIR14 Nucleotide Sequence (SEQ ID NO:27)**

ATGAGCGCCGCCCTGGGTCCGGCGTTCCGCCCTGACGCCGATGCCGCCCTGCCCTGCCCTGCTTCC  
 CCCATGCAGGGGGCAGGCCAGCTCTTCCGTAGCTGGAGCGAACGCCCTGCCGCCAGACATCGACCT  
 GCTTGCCTGCCAGTACCCGGGTCCGGAGGACCGCTCAACGAGGCCGCCACCCGCCCTGGAGGAC  
 CTCGCCAGGGGCCGCCCTGCCCTGCCGATTTCGCCGACGCCGCCCTGGCGCTTCCGCCACA  
 GTCTCGCGCGGCCGCTGCCCTACGAAACGCCCTGCCCTGGAAAGGCCGCCGCGCCGCTGCC  
 CCTGTTCGTCTCCGCCATCCGGCACCGCACCGCAACCGGGCGGCCGCGCTTGACCCGCCGACGAG  
 CGCGCGCTGCTGGAGGACGTCCGCCAGGGTGGCGCCAGCGAGCTACTCGAGGACGCCGACCTGC  
 CGCGCTGTTCCCTGCCGATCCTGCCGCCGACTACCAGGCGATCGAGACCTACCGACGGCGCAGCC

CATGCCCTGGCCTGCGCCCTCGACGTCTCTCGCGGAGCACGACGAGGAAGTCAGGCCGCCAG  
GCGCAGGCCCTGGAGCGACGCCAGCCGGACTCCCGCAGGCTCGGGCTTCTGGCGGCCACTTCT  
ACCTGAGCGAGGGGCGCGACCGCGTATCGAGCACCTGCTGCGCCCTCGCACATCCCACGCCCT  
TTCCCGAGAGGTTGCATGA

The VIR14 protein (SEQ ID NO:28) encoded by SEQ ID NO:27 is presented using the one-letter amino acid code in Table 16B.

**Table 16B. Encoded VIR14 protein sequence (SEQ ID NO:28)**

MSAAWVRPFRLTPMPRLRLACFPHAGGSASFFRSWSERLPPDIDLLALQYPGREDRFNEAPATRLEDL  
ADGAALALRDFADAPLALFGHSLGAALAYETALRLESAGAPLRLFVSAHPAPHRQRGGALHRGDEAA  
LLEDVRQGGASELLEDALRALFLPILRADYQAIETYRRAQPIALACALDVLLGEHDEEVSAEAQA  
WSDASRTPARLRRFPGGHFYLSEGRDAVIEHLLRLAHPDALSREVA

5

### MUT15

A *Pseudomonas* bacterial mutant (MUT15) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydroaeruginoic acid synthetase pchE (PA4226). This gene encodes the VIR15 nucleic acid (SEQ ID NO:29) shown in Table 17A.

**Table 17A. VIR15 Nucleotide Sequence (SEQ ID NO:29)**

ATGGATCTGCCCTGGATTCGGTACCGCCCTGCGCAGCTGGTGGACGGAGCAGCTGCCGACCTGC  
TCGGCGAACCGCTTGTGACGTGCGCCCTGGCGGACGACGACGACCTGCTGGGCTGCGGCCCTCGA  
CTCGATCCGCTTGTGACCTGCGAGAACGCCCTGCGCGCGTGGCTCGACGCTGGACTTCGCCAG  
TTGGCGCAGGCCCTGCGCTGGCTGGGGCTGGCTCGACACTGCTGGCGCGGACCGGCTGCGGCC  
CGGCAACGGTGCCTGCCGACGGCGCAGGATCGCAGTCAGCCGTTGGAGCTGCTTCCGTGAGCA  
GGCTACTGGCTGGGACGTGGCGCCGGCAGGGTGTGGCACGTCAGCTGCGCATGCGCTTCTGGAA  
TTCCGCACGGGGATGTCGACCCGAGCGCCTGGCGGGCGAGTGCCTGCGTCAACGCCACC  
CGATGTTGCGGGCGCGCTTCCTCGACGGTCGCCAGCAGATCTCCGACGCCGCGCTGCTGCTT  
CGACCTGCAGGACTGGCGCACCTACAGGTGGACGAGGCCAGCGCGACTGGCAGGGCGCTGCGCAG  
TGGCGGCCATGAATGCCCTGGCGGTGGAGCGCGGCCAGGTGTTCTGCTCGGGCTGGCGCATGC  
CGGGCGGCCAGGGATCGCCTCTGGCTGAGTCTCGACCTGCTGCGCCGATGTCGAAAGCTGCGCCT  
GCTGCTGGCCGAACCTGGCGTGGCTACCTGGCGCCGGAGCGCCTGGCGAGGCCGCCGGCGCTGCAT  
TTCGCCGAACCTGGCGCACCGTGGCGCAACCGCGCCGAGGCCGCCGGCGACTACT  
GGCTGGAACGCCCTGCCGCCCTGGCGGCCAGGCCGCCCTGCGTTGGCTGCGCGCCGAAAGCAT  
CCGCCAGCCGCGACCCGGCGCTGGCATTCGACCTTCCGCGCCGGAGAGGCCGCCCTGGAGCGT  
CTTGGCGCGCAGCATGGCGTGACCTTGTCCAGCGTGTCCGCTGCCCTCGCGCTGGCTCTGGCGC  
GCTGGAGCGAAAGCGCGGAATTCTCCCTAACGTGCCGTTGTCGATGCCATGCCGACGACCCGCG  
TATCGCGAGGTGATGCCGACTTCACCAACCGTGTGCTGCTGGAGTGCGGATGCAAGGCCGGT  
TCCTCGCGAGGCAGGTGAAGAGCTTCCAGCGCAACCTCCACGGAGCCATCGACCCGCGATTCC  
CCGCCCTGGAGGTGCTCCCGAGGGCGCCGGCAGGGCAGCCACGCGCTGGCGCCGGTGGTGTTCGC  
CAGCAACCTGGCGAGGGCTTCGTCCCGGCCCTTCCCGGACGCTTCCGGAGTCTCCACGAC  
ATGCTCTCGCAGACCCCGCAGGTCTGGCTCGACCACTAACCGGTTGGCGACGGTATCCTGC  
TGGCCTGGGATAGCGTCGTCGGCTGTTCCCGAAGGTCTGCGGAAACCATGTTCGAAGCCTACGT  
GGGCTGCTCCAGCGTCTGCGACAGCGCCTGGGGCAGCCCCGCGATCTGCCGTTGCCCTGGCG

CAGCAGGGCGCCGGGCCCTGCTAACGGCCAGCCGCATGCGCCACGGCGGCACCCGATCGGC  
 ACTCTTCTTCGCGCCCGAGGCAGCCGGATGCCGACCGCTGCTCTATCGGACCAACGGTGTAC  
 CGCGCGCGAAGTGGCGAGCGTGCCTGCGCATGCCGGCGCTGCGGAAGCGGGGTGCGCC  
 GGCACGCGGGTCAAGGTCAGCCTGCCGCGACCGCAGCAGTCCGGCGGTATTGGCGTGC  
 CGCAGGGCCTGCTACGTGCCCTGGACATCGACCAGCCGCCGACGGCGGCCGATCGAAGA  
 GGCGCCGGGTATGCCGATCACCGAGGAGGACGATCCGAGGCGCTTGCGGCCGCGCTGG  
 GTCAGCGCTGCTGCCGGCGCTGGCGCCCGTGCCTGGCGCCGAGGCGAGTGCCT  
 ATGTGATCTACACCTCGGGCTCCACCGGGTGCACGGGCGAGGGCGTGCAGCCACGCG  
 CAATACCATCGACGCGCTGCTGACCTGCTGCCGGTGAACGACATCGGATCGCTGGCG  
 GCGTGGACTTCGATCTGCGGTCTCGACCTGTTGCCGGCTCCGGCGCCGGTGC  
 TGCCGGCCAGGAACAGCGCGATGCCGCTGCCCTGGCGGGAGGCTATCCAGGGCATGCG  
 CCTGTGGAACTCGGCAGGGCCTTGCTGGAGATGGCCCTCAGCCTGCCGGCGACGGCG  
 CGCAGTCTGCGGGCGGTGCTGCTGCCGGCACTGGGTGGCCCTGGACCTGCCGGCG  
 CACGTTGTGCCGAAGGCTGCCGCTGCATGTCTGGGTGGCGTACCGAAGCGGGCAT  
 CCTGCAGAGCGTCGATAACGGTGCCCGCACTGGCTTCGATTCCACGGCCGGCAT  
 CAGGCCAACCGGGTGGTCGACACCCACGGGCGGACGTGCCGGACCTGGTGGCG  
 TGCGGGCGCAGGCTGCCGGCGCTATCGCAACGATCCGAACTCAGGCCGGCGTT  
 CGATGCCAACGGGCCAGGCTGGTATCGCACCGGGGATCGCGGTCGCTACTGGGCG  
 TTCTCGGTGGTGCACAGCAGGTGAAAGTGCAGGCCAGCGCATCGAGTTGGCG  
 CGCGCTGTGCCAACGGCTGGCGAGAGGCCCTGCCGGCGGTGCTGGCG  
 CCTGGCGCGGTGCTGGTACCGCGCTGCCGGCACGGGCCAGGGCAAGGCT  
 CAGCCCTTCGCCGGCGCTGCCAGAGGCCGAGGCCGTTACCA  
 AGGCAGGCTGGAGCTAGACGACGGTTGCCGGCGCTGGCTGGACTGG  
 CAGCGCGCTGCCGCTCGACGAGCGTTGCCGGCTGGCTGGCG  
 ATGGGCAACGCTCTGCCGGCTGCTGCCGGGAAACAGGCGCCGGCG  
 GGCTGGCGCCGCAAGCGGGTGGCGCGCCTGCCGGACGGCG  
 AGCGCTGCCGACGCCGGCTGCCGGCAACGCC  
 TGGCTCGACCGGGATGGCTCGCTGTTGCCAGGGCTGGAA  
 ATGGGCAACGCTCTGCCGGCTGCTGCCGGGAAACAGGCGCCGGCG  
 GGCTGGCGCCGCAAGCGGGTGGCGCGCCTGCCGGACGGCG  
 AGCGCTGCCGACGCCGGCTGCCGGCAACGCC  
 TGGACCTGCTATGCGAGTCGCCACTGGCGCTGCTGGCG  
 CCTGGCGAGCTGCCAGGCCCTGGCGAGGCGCTGGAA  
 CGCAGCGAGCGGATGCCCTGGCGAGGCGCTGGCG  
 AGGCCGGCTGGAGCAAGGCCCTGCCGGCAAGGCC  
 GCCGTTGAACGGAATGCAAGGTGATGCGGCCCTGGCG  
 GAGTGTGTCACGAGGCCCTGCCGGAGGAGGCC  
 GGGAGCGGTTCTCAAACGCCGGTGCCTGCCAGGG  
 CCTGCTGGCGACCCGCTGCTGGCG  
 TTCTGCGCTGAGCTTCCAGCTCGGCCG  
 TTCTGCGCTGAGCTTCCAGCTCGGCCG  
 AAACCAACTGGAAGAGGGCGTGTATGA

The VIR15 protein (SEQ ID NO:30) encoded by SEQ ID NO:29 is presented using the one-letter amino acid code in Table 17B.

Table 17B. Encoded VIR15 protein sequence (SEQ ID NO:30)

MDLPPDSRTALRDWLTEQLADLLGEPLADVRALADDDLLGCGLDSIRLMYLQERLRARGSTLDFAQL  
 AQRPLCGAWLDLLACADRLSAPATVALPTAQDRDQPFEVSSVQQAYWLGRGAGEVLGNSCHAFLEFR  
 TRDVPDQRLAAAECVRQRHPMLRARFLDGRQQLPTPPLSCFDLQDWRTLQVDEAERDWQALRDWRA  
 HECLAVERGQVFLGLVRMPGGEDRLWLSSLADLVAESLRLLAELGVAYLA  
 PERLAEPPLAHFADYLAHRAAQR  
 AARARDYWLRLPRLPDPAPLPLACAPESIRQPRTRRLAFQLSAGESRR  
 LERLAAQHGVTLSSVFGCAFALVLARWSESAEFLNVPLFDRHADD  
 PRIGEVIA  
 DFTLLL  
 LECRMQAGVSPAEAV  
 KSFQRNLHGAIDHAAPALEVLREARROGQPR  
 SAPVVFASNL  
 GEEGFVPAAFRDAFGDLHD  
 MLSQTPQ  
 VWLDHQLYRVGDILL  
 AWD  
 SVVGLFPEGL  
 PETMFEAYVGL  
 QRLCDSAWGQ  
 PADLPLPWA  
 QQARR  
 ALLNGQ  
 PACATARTL  
 HRDFFLRA  
 AEP  
 DAD  
 ALLYR  
 DQR  
 VTR  
 GELA  
 ERL  
 RIAG  
 GL  
 REAG  
 V  
 R  
 P  
 G  
 D  
 A  
 V  
 E  
 V  
 S  
 L  
 P  
 R  
 G  
 P  
 Q  
 V  
 A  
 A  
 V  
 F  
 G  
 V  
 L  
 A  
 A  
 G  
 C  
 Y  
 V  
 P  
 L  
 D  
 I  
 D  
 Q  
 P  
 P  
 A  
 R  
 R  
 L  
 I  
 E  
 E  
 A  
 A  
 G  
 V  
 C  
 L  
 A  
 I  
 T  
 E  
 E  
 D  
 D  
 P  
 Q  
 A  
 L  
 P  
 P  
 R  
 L  
 D  
 V  
 Q  
 R  
 L  
 L  
 R  
 G  
 P  
 A  
 L  
 A  
 P  
 Q  
 A  
 S  
 A  
 Y  
 V  
 I  
 Y  
 T  
 S  
 G  
 S  
 T  
 G  
 V  
 P  
 K  
 G  
 V  
 E  
 V  
 S  
 H  
 A  
 A  
 I  
 N  
 T  
 I  
 D  
 A  
 L  
 L  
 D  
 L  
 R  
 V  
 N  
 A  
 S  
 D  
 R  
 L  
 L  
 A  
 V  
 S  
 A  
 L  
 D  
 F  
 D  
 L  
 S  
 V  
 F  
 D  
 L  
 F  
 G  
 G  
 L  
 G  
 A  
 G  
 A  
 S  
 L  
 V  
 L  
 P  
 A  
 Q  
 E  
 Q  
 A  
 R  
 D  
 A  
 A  
 A  
 W  
 A  
 E  
 A  
 I  
 Q  
 R  
 H  
 A  
 V  
 S  
 L  
 W  
 N  
 S  
 A  
 P  
 A  
 L  
 L  
 E  
 M  
 A  
 S  
 L  
 P  
 A  
 S  
 Q  
 A  
 D  
 Y  
 R  
 S  
 L  
 R  
 A  
 V  
 L  
 L  
 S  
 G  
 D  
 W  
 V  
 A  
 L  
 D  
 L  
 P  
 G  
 R  
 L  
 R  
 P  
 R  
 C  
 A  
 E  
 G  
 C  
 R  
 L  
 H  
 H  
 V  
 L  
 G  
 G  
 A  
 T  
 E  
 A  
 G  
 I  
 W  
 S  
 N  
 L  
 Q  
 S  
 V  
 D  
 T  
 V  
 P  
 P  
 H  
 R  
 S  
 I  
 P  
 Y  
 G  
 R  
 P  
 L  
 P  
 G  
 Q  
 A  
 Y  
 R  
 V  
 V  
 D  
 T  
 H  
 G  
 R  
 D  
 V

PDLVVGELWIGGASLARGYRNDPELSARRFVHDAQGRWYRTGDRGRYWGDGTLEFLGRVDQQVKVRGQ  
 RIELGEVEAALCAQAGVESACAAVLGGGVASLGAFLVPRLAPEAGSMDLPAAQPFAGLAEAEAVLTER  
 EILGALLEAPLELDDGLRRRWLDWLADSAASALPSLDEALRRLGWQAAGLTAMGNALRGLLAGEQAPA  
 ALLLDPWLAQAVAARLPEPDGREALARLLEALPTPAAGERLRAVLDTRAGLWLDQGMASLRLPQGLELT  
 LFERSRVLLDAAAATRLPERIVVQALDDGLLPAEHLGRYDRVISFAALHAYEASREGLALAALLRPQG  
 RLLLVDLLCESPLALLGAALLDDRPLRLAELPSLLADLAAGLAPRCLWRSERIALVEALAPGLGLDA  
 AALQAGLEQRLPQAMRPERLWCLPSLPLNGNGKVDRRRLAESMTRALGECHRHEPSAEEPLEAHEQALA  
 ECWEAVLKRPRRREASFFSLGGDSLLATRLLAGIRERFGVRLGMADFYRQPTLAGLARHLQVQTVEI  
 EETQLEEGVL

## MUT16

A *Pseudomonas* bacterial mutant (MUT16) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin synthetase pchF (PA4225). This gene encodes the VIR16 nucleic acid (SEQ ID NO:31) shown in Table 18A.

**Table 18A. VIR16 Nucleotide Sequence (SEQ ID NO:31)**

ATGAGCCTCGCGAAGCTGCTGGAAACCTGCCAGCCGGCGATCGAACTCTGGAGCGAGGCCGGCC  
 GCCCTGCGCTATCGCGCCCCCCCAGGTGCCCCCTCGACGCCGGCCTCGCCGAGCGCCCTGCGGGCCGAGCG  
 CGAGGCCCTGCTGAAACACCTGGAAGCGGGCCCTGGCTGGCGCGCAACCCGACATGGCCACCAG  
 CGCTTCCCGCTGACCCGGTGCAGGCCGCCTACGTCTGGGCCGCCAGGGCGGCTTCGACTACGGCG  
 GTAACGCCCTGCCAGCTGTACGCCAGTACGACTGGCCGGCGACACCAGTCGGCGGCCCTGGAGGC  
 GGCTTGGAAACCCATGGTCAGCGCCACCCGATGCTGCGCGCGTATCGAGGACAACGCCCTGGCAG  
 CGCGTCTGCCCAGGGTGCCTGGCAGCGGCTGACCGTGCATGCCCTGCGGGCTCGACGAGGCC  
 CTTTCCAGGCCACCTGGAGCGGGTCCCGCAACGCCCTCGACCACGCCCTGCGGGCGCTGACCAAGTG  
 GCCGGTCTCGCGCCCGAGCTGAGTATCGGCCGGGATGCCCTGCGTACTGCACTGCTGGTGGATTTC  
 ACCCTGGTCGACTACGCCAGCCCTGCAATTGCTGCTGGCGAATGGCGCCGCCCTATCTCGATCCGC  
 AATGGACGGCGGAACCGCTGGAGGCACCTCCGCACTATGTCGGCTCGAGCAGCGCCACGCCA  
 GTCGCCAGCTGGCAGCGCGACCGCGACTGGTGGCTGGCGCTCGACCGCCTACCGGGCGTCCC  
 GACCTGCCGCTGCGGTGCAAGCCGGACACCCGGTCCACCGCCTCCGGCACTTCCACGCCGCGCTCG  
 ACGAGGCCGCGCTGGCAGGCCGCTCGGCCGCGCCGGCAACACGCCCTGAGCGCTGCCGGCGTGGC  
 CTTGGCGGCCCTCGCGAGACCATCGGTGCTGGAGCCAGGCACCGGGTTCTGCTCAACCTGACG  
 GTACTCAACCGGCCGCCCTGCATCCGCACTGGCGCAGGTGCTCGGTACTTCACCGCGCTCAGCC  
 TGCTGGCAGTGGACAGCCGCCACGGCAGCTTTCGTCAGCGCGTCGACCTGCTGCCGGAACCTGGCGCCGGT  
 GTTCGACGACCTCGACCACCCGACCTTCAGCGCGTCGACCTGCTGCCGGAACCTGGCGCCGGT  
 GGTGCGGGCGCCGATCTGATGCCGGTGGTCTACCAGTGGCATCGGCAGCGTGCAGCGCTGCTCG  
 GCGATGGCGAGGCCGCCGCGCGCACGCTACATGATCACGCCAGACCCCGCAGGTCTGGCTGGACTG  
 CCAGGTCAACCGACCAAGTTCGGCGGCCCTGGAGATCGGCTGGGACGTACGCCCTGGGTTGTTCCCGAG  
 GGCCAGGCCGGAAGCCATGTTGACGACTTCGTCAGCGACTTCGTCGGGCTGCTCCGGCGCTGGCGCAGAGGCCGCG  
 CCTGGACCGACGGCAGGCCACGGAACCCGTCAGGCCGCCGCGAGCGTGGCCGGTAGTGGCCCG  
 GAGCATGCCGCCGGTTTCGCCAGCGTGGCCCTGCTGACCCCCGACGCCAGCGCATCCACGATGCC  
 GCCCGCAGCTACAGTACCGCCAGGTGCCCCAGCACGCCAGCGCCCTGCCCGCTGGGACTG  
 ACGGCGGGCCGTGGCGGGTCGCGGTGATGCTGCCGAAAGCGCCGCCAATTGGTCGGCGT  
 GATCGGCATCCCTCAGGCCGGCGCCGCTATGTCGGTGGACATCCGCCAGCCCTCCGCTGCCGCG  
 CAGGCCGATCCGCCAGGCCGAAGTGGTCGCCGCTGGTCTGCCCTGGAAAGCGATGTCCCAGCG  
 GCTGCGCTGCCATCGACCAGGCTGGCCGACAGCGCCTGCCGCCACCGCCGCCGG  
 GGTGGCGGGACGACCTCGCTACGTGATCTACACCTCCGGCTCCACCGGACGCCAAAGGGCGTG  
 ATGCTCAGCCATGCCGGGTGAGCAACACGCTGCTCGACATCAACCAGCGCTACGGCGTCAGGCCA  
 ACGACCGCGTCTCGGCCAGGCCGAAGTGGTCGCCGCTGGTCTGCCCTGGAAAGCGATGCTCATCGATT  
 CGCGCGGGGGCCAGTGGTCTCCGGACCCGGCGCGCCAGCGATCCATCGCACTGGCGGAA  
 CTGCTGGAAACGCCACGCCATCACCCCTGTGGAACTCGGTGGCCGCCAAGGCCAGATGCTCATCGATT  
 ACCTGGAGAGCGAGGCCAACGTCACCTGCCGGACCGCGCTGCCGCTGCTGGTCCGGTACTGGAT

TCCGGTCAGCCTGCCGACCCGCTGGTGGCGGCTGGCCGGACAGCGCGCTGTTAGCCTGGCGGC  
 GCCACCGAGGCGGCGATCTGGTCGATCGACCGAGCCGATCCGCCCGAGCACACCGAGCTGGCCAGCA  
 TCCCTTATGGCGTGCCTCGCGGGCAGAGCGTGGAAAGTCTGATGCCCGGGCTGGCGCTCGGCTACGCCGGCAGTC  
 GCCGGCGTGCAGGAGATCCATATCGGCGGGTGGGCCTGGCGCTCGGCTACGCCGGCAGTC  
 CAGCGCACCGCCGAACGCTTCGTCACCCGATGGCGTGCCTGATGCCACCGGCAGCTCG  
 GCCGCTACCTGGCGACGGCAGCAGTCAGGTTCTCGGCCGAGGACGACCAAGGTGAAGATTCGCGG  
 CCACCGCATCGAACTGGCGACTGGACGCCGCTGCGCTCATCCGAGGTCAACCTGGCGGC  
 ACCGTGGTGCCTGGCGAGACCCACGAGCGCAGCCTGGCAGCTTCGTCACCCCTGCATGCCCGGTGG  
 AGGCTGGCGAGGAGTCCCGTACGGCGTCAGCGCGTGGCGCAGCGGGCGCCAGGCCTTGCAGCG  
 CGACTGGGGCAGCGAGGGCATCGCCGCGGGTGGCGACTCGACCGTGCCTGCCCTCG  
 TTGGCCGCTGGCTGGCGAGCGGTCTGTTCCAGTGCAGGCCGCTGGACTTAGCCACCCCTGT  
 GCCAGCGCTGGTATCGCCGAGGGCGCCAGCGCCTGTCAGGCCACTGGTTGCGCCAAGTGGAGGA  
 GGGCGCTACCTGCGCGCCGAGGGCGAGGGCTGGCTGGCTGCGCCAGCGTCCCGCGCAGAGTCCCG  
 GAGGACGCCCTGGACGGCGTTCGCGGGCTGCGCGCCGGCGCTTGGCCGGGAGCTGGTGCCT  
 ACCTGCGTACAGCGCGAATCCCTCGCGAGCAACTGCCGGGGGATCAGCCCAGGGCGGCTGT  
 GTTCCCGCAGGGCTGGCGCATCGCGAGGCCATGTACAGCCAGGGCCTGCATGCCAGGCCTG  
 CACGAGGCCATGGCGAGGCCATCGCCGCCATCGTCAGCGCCAGCGCAACGGCGCTGGCGCTG  
 TGGAGCTGGCGCCGGCACCGCCGCCAGCGCACGGTATCGCCGGTGGCGCTGGTGCAG  
 GCGAGGGCGGAGGTGGACTACCTGTTACCGACGTTCCAGCTACTTCCTCGCCGCCGCGAG  
 CGCTTCCCGGACCAGCGCTGGTACGCTTCGCGCTTGACATGAACGGCGATCTCTGACCAAG  
 GCGTGGCGCCGACTCGGTTGGATATCCTGTCAGCTCCGGGCTTGAACAAACGCGCTGGACACCCC  
 GCGCCTGCTGGCGGCTGCGCAGTTGCGTGAAGCGCCAGCGCTGGTGGTGAATCCAGGAAC  
 CGCAGCACACGAGATCAGCGTCAAGCCAGAGCGTGTAGTGGAAAACCCGCGGACCTCCGCGACG  
 AGCGCCGCAACTGTTCGTCCACACCGGCAATGGCTGGAGTGGCTGGGGCACAGGGTGGCGACCT  
 GGCTTGTGGGGTGGTGCCTGGGGAGCGCTCTGACCTGCTTGGCTACGATGTCCTGTCGGCTCG  
 TGCAAGACCGACCAGCGCCGCCCTGGAGCGCCGGAGCTGCTGGCTTCGTAAGCGCGGGTGC  
 GCTACATGCTCCCGCGCAGTTGCGCGTCTGCAACGCCGCGTCAACGGCAACGGCAAGATCG  
 CCGCAAGGCCCTGACCGGCTTGGCCAGCCCCAGCGGACCTCGGCATGGCGTCCGAGGCA  
 CCGCCGACGAACTGGAGAATGCGCTGCTGGCACTCTGGCGGGAGGTGCTGGACAAACCGCTG  
 GCGTCGAGCAAGACTTCTCGGGGCGGCGACTCGCTGTTGATCGCCCAGTTGATGCCCGTT  
 GCGCGAACGACTGGAAAGCGCCGCTGGCATCCGTTGATCGCCTGCTACGCTGGCGCTCAG  
 CCGACGCCGCGGGCTGGCGAACGCCCTGCGCAGCGCCGGAGAGGGCGTGGCGCAGCCCTGG  
 CGCGCGCGCGGGCTGGCCCCGGGGGGGGCATGTCGCGCAGCGCTCGCGAGGGCGCGGT  
 GCGCCTGACCCGCTGGCGCTGGCGCCCCGGGGGGGGCATGTCGCGCAGCGCTCGCGAGGGCG  
 CTGGCGACCGCTACTGCGTACCGCCGCTGCTCGCCGCCCCGGGGTGGTGAAGGGCGCCGTT  
 TGGCGTGCATGACAGCGACGCCAACCTGGCGATCCCCGGGAGCATCTAACGCCCTGCC  
 CGCTACGCCGAGGCCTCCATCGCGCCGGGCTACGCGAGGTCGACCTGTCGGCTACTGCT  
 GGGCTGGTGCCTGGAGACGCCAACGCCCTGGTCCAGCGCGGGGTGCGCGTGCCTGG  
 TCGTCTCCAGCTACCGGATTCCCTACCGGGTGGACGACCGAGCGCCCTGCTGTTGTT  
 GACCCCTCGGCTGGATACCGCGCGCTCGGCTTCCCCGCCGGAACGCTCTGGCCAGGGCG  
 GCGCGCTCGCGCAGACACCGGAGCGCTGGTCGCCGAGGCCTGGCGGGGCTGCC  
 ATCTCGTGCCTGGCGGGGGCGTGTACAGCGGCCAGCGGTAGCGCCGACGCCGTCAGCG  
 ACAGCGACACCCCTACCGGCTGGTCACTCGGTGCGCAGCCAGGCCAGGCCGGAGGCC  
 TACGGTGGCGCGCTGGCGTGTGCGGGAGGCCGGAACCCATGGTGGCCCGCTACGCC  
 CTCTGGAGACCCAAATGGCGGGCCGCCGCTGGCGTGCCTGGCGCATCCACGAGGT  
 CTTCGACTGCCCTGGCGAAGCCCTGGCGCAATCCTGTCGAACCCATGCCAGAGGAGGG  
 GAGCCGA  
 TGA

The VIR16 protein (SEQ ID NO:32) encoded by SEQ ID NO:31 is presented using the one-letter amino acid code in Table 18B.

**Table 18B. Encoded VIR16 protein sequence (SEQ ID NO:32)**

MSLGELETCRSRRIELWSEAGRLRYRAPQGALDAGLAERLRAEREALLEHLEGGPGWRAEPDMA  
 HQRFPLTPVQAAVVLGRQAAFDYGGNACQLYAELYDWPADTDPARLEAAWNAMVERHPMLRAVIED  
 NAWQRVLP EVPWQRLTVHACAGLDEAAFQAHLERVRERLDHACAALDQWPVLRPELSIGRDACVL  
 HCSVDFTLVDYASLQLLLGEWRRRYLDPQWTAEPLEATFRDYVGVEQRRRQSPAQRDRDWLAR  
 LDALPGRPDPLRVQPDTRSTRFRHFHARLDEAAWQALGARAGEHGLSAAGVALAFAETIGRWS  
 QAPAFCLNLTVLNRPLHPQLAQVLGDFTALSLLAVDSRHGDSFVERARRIGEQMFDDLDHPTFS  
 GVDLLRELARRRGRAADLMPVFTSGIGSVQRLLGDGEAPRPRYMIQTPQVWLDCQVTDQFGG

LEIGWDVRLGLFPEGQAEAMFDDFVGLLRRAQS PRAWTGDATEPVEAPPQALPGSARSTIAAGF  
 AERALLTPDATAIHDAAGSYSYROVAQHASALRRVLEAHGAGRGRVAVMLPKSAAQLVAVIGIL  
 QAGAAAYVPVDIQRQPLRRQAILASAEVVALVCLESVDVGCACVAIDRLAADS AWP PPPAAEVA  
 ADDLAYVIYTSGSTGTPKGVMLSHA AVSNTLLDINQRYGVDANDRVLGLAELSF DLSVYDFFGAT  
 AAGAQVVLPLDPARGSDPSPHWAELLERHATLWNSPQAQGQMLIDYLESEPQRHLPGPRCVLW SGD  
 WI PVS LPT RWW RWPDSALFSLGGATEAAIWSIEQ PIRPQHTELASI PYGRALRGQSVEVLDARG  
 RRCPPGVREGEIHIGGVLALGYAGDPQRTAERFVRHPDGRRLYRTDGLGRYLA DGSIEFLGREDD  
 QVKIRGHRIELAELDAALCAHPQVNLAATVVLGETHERSLASFVTLHAPVEAGEDPRTALDAV RQ  
 RAAQALRRDWGSEEGIAAAAVALDRACLASLAAWLAGSGLFASATPLDLATLCQRLGIAEARQRL  
 LRHWRQLEEGGYLRAEGEGWLGC AERPAQSPEDAWTAFA GCA PAALWPAELVAYLRDSAQSLGE  
 QLAGRISPAALMF P QGSARIAEAMYSQGLHAQALHEAMA EATAI AVERQPQ RWRLL ELGAGTAA  
 ASRTVIARLAPLVQRGAEV DYLFTDVSSYFLAA RERFADQPWVRFGRFD MNGD LLDQGVAPHSV  
 DILLSSGALNNALDT P ALLAGLRELLSADAWLVIQELTREHNEISVSQSLMMENPRDLRDERRQL  
 FVHTGQWLEWLAAQGGDLACGVVPPGSALDLLGYDVLLARCKTDARLEPAELLA FVEARVPRYM  
 LPAQLRVLERLPVTGNGKIDRKALTG FARQPOADLRHGVQA QAPADEL NALLWREVL DNP SLG  
 VEQDFFGAGGDSLLIAQLIARL RERLESARRH PFD RLLRWALSQPTP RGLAERL RSAPEEGRGPA  
 LAAARGVAPAPAGMSRAPLAEGAVALDPLVRLVPGEGVPRVLVHEGLGTLLPYRPLL RALGEGRP  
 LLGLAVHDSDAYLAI PAEHLNA CLGRRYAEALH RAGLREVDLLGYC SGGLVA LETAKSLVQRGVR  
 VRQLD IVSSYRIPYRV DDERLLLF SFAATLGLDTAALGF PAPERL GQAVQ AAL AQT P ERLV A EAL  
 AGLPGLADLVALRGRLQ AASGSADAVSVERDTLYRLFCHSVRASQAEAP E P YVGA LRLF VPDAG  
 NPLVPRYAE ALETQWRAA ALGACGIHEVPGGF DCLGEAL AQSLSKPMPEASR

## MUT17

A *Pseudomonas* bacterial mutant (MUT17) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding putative ATP-binding component of the ABC transporter, pchH (PA4223). This gene encodes the VIR17 nucleic acid (SEQ ID NO:33) shown in Table 19A.

Table 19A. VIR17 Nucleotide Sequence (SEQ ID NO:33)

GTGACCCCGGTGCTGTGGCGCCTGCTGGCACCTATCGCTGGCGGCTGGCGGGCCATGGGGTTGC  
 AGGCCCTGGCCGGGCTCTGCTCGCTGTTGCCCTGGATGCTTCTCGCCTGGCTCGCCGAGCCGCTGGC  
 GCGCGGCCAGGCGCAGCCGGCCCTGCTGGCCCTGGTGCCTGCTGGCGGTGCTGGCTGGCTGGCTGGCTGC  
 CAGGGCGCTGGCCCGCGCACCTGGCCACCCGGGTGACGCGGACCTCTGCAACGACCTGCGCCTGC  
 TGCTGGCGCACCTGCAACGGCTGGCGCTGGACTGGTTCGGTGCGCCAGGGCCCGACGGCGTGGCG  
 CCTCGTGGAGCAGGAGCTGGCGGCCCTGCAACCAACTGATCGCGCACGCTCCAAACGATCTCAGCAAC  
 CTGTTGGTGGTGCCTCGCGCTGCTGGCTGGCTGGCTGGCGTGCACCCCTGGCTGCTGCTGTTCT  
 GCCTGCTGCCGCTGGTGCCTGGCCGCCGCGCTTCCTGCTGCTGCCGCTGGCTGCCGCGCTACCGCGACCT  
 GGTGCTGCCGCGCACCGCGCGCTGGAAAGGCTCTGGCGGACTATGGCAATTGCCAACAAACCTG  
 CTGCTGGCCCGACAGTACCCCGGCCGGCATACAACAGGGCGCCGAGGCGTGGCGGCCGCTTC  
 GCGAAGCGTTGGCGCCTGGGTGAAGCGGGTGGCCACCTCGCCGCCGCTGGTCTACGTCAGTTGTC  
 GACGCCCTGGCTGCTGGCCTGGGTCTGCTGGCGCGCTGGCCCTGGATGCCCTGGCGTGGCGCTG  
 GCGCTGGCCAGGCCCTGTGCCCTCCCTGCTCTGCTGCCGCGCTGGCTGCCCGGTGCGAGGCGCTCG  
 GCCACGGCGCGACGCGCTGCTGGCGCGCGGCCGCGAGCGCCTGCAAGCAGGTGTCGACCA  
 GGC CGCGCTGGCCGAGGGCGCTGCAACCGCGAGCCGGTCGATGGCGCGTGGCGCTGCACGGCG  
 GGCCATGCCATGAAGGGCTGGAGGTCCTGGCGATATCGATCTGGAGCTGGAGGATGGCAGCCTGG  
 TGGCCCTGGTGGTCCCTCGGGCTCCGGCAAGAGCACCCTGCTGCACCTGCTGGCGCGTACATGGA  
 CGCGCAGCGCGCGAACTGGAGGTTGGCGGCCCTGGCACTGAAGGACATGCCCTGATGCCGTGCGCCAT  
 CGGCATATCGCGCTGGTGGCCAGCAGGCGCGCGCTGGAGATATGCCCTGGCGACAAACATTGCCC  
 TGTTCCGCCCGATGCCGATCTCCAGGAGATTGCCAGGGCGCCCTGAGCCTGCCGACGAGCG  
 CATCATGGCCCTGCCCGTGGCTACGACAGCGTGCCGGACGCGACCTGCAACTGTCCGGCGAA  
 CTGCAACGACTGGCCCTGGCCGTGGCTATGCCGGCAGCCTGTTGCTGCTGACGAGCCAA

CCTCGCGCTGGATCCGAGACCGCCGGCAGGTCTGGCAACCTGGCGAACGGCGGGTGGCG  
GACCCGGGTGATCGTCGCCATCGTCTGGCGAAGTCAGCGATGCCACCTGATCCTGGCTGGTC  
GCTGGCGTCTGGTCGAACGCCGAGCACGCCGCTGTTGGCGGACGCCATGCCGCT  
TGTGGCGTGAACAGAACGGCGGGAGGTGGCGGCATGA

The VIR17 protein (SEQ ID NO:34) encoded by SEQ ID NO:33 is presented using the one-letter amino acid code in Table 19B.

**Table 19B. Encoded VIR10 protein sequence (SEQ ID NO:34)**

MTPVLWRLRLRTYRWLAAAMGLQALAGLCSLLPWMLLAWLAEPLARGQAPALLAVLLAVLAWL  
GCQALAAHLAHRVDADLCNDLRLRLAHQLRLPLDWFGRQGPDVARLVEQDVRLHQLIAHAPN  
DLSNLLVVPLVALLWLAWLHPWPLLFCLLPLVLAAGFLLRSARYRDLVLRRNAALERLSADYG  
EFAHNLLLARQYPGAGIQQGAEASAAAFGEAFGAWVKRVGHLAALVYVQLSTPWLLAVVLLGALA  
LDALGVPLALQACAFLLLRLAALPQVQALGHGGDALLGARAAAERLQQVFDQAPLAERSTREP  
VDGAVALHGLGHAYEVLEADIDLELEDGLSVALVPGSGSKSTLLHLLARYMDAQRGELEVGG  
LALKDMPDAVRHRHIALVGQQAALEISLADNIALFRPDADLQEIRQAARDACLDERIMALPRGY  
DSVPGRDLQLSGGELQLARALLSPASLLLDEPTSALDPQTARQVLRNLRERGGGRTRVIVA  
HRLAEVSDADLILVLVAGRLVERGEHAALLAADGAYARLWREQNGAEVAA

5

The role of VIR17 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

### MUT18

10 A *Pseudomonas* bacterial mutant (MUT18) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the putative ATP-binding component of ABC transporter, pchI (PA4222).

15 This gene encodes the VIR18 nucleic acid (SEQ ID NO:35) shown in Table 20A.

**Table 20A. VIR18 Nucleotide Sequence (SEQ ID NO:35)**

ATGACCCCTGTTCGAACGAAATGCGTGGCCTGCCCGAACGACTGCCGTGCCGGCTTGC  
CCTGGCGGGTCTGGCGGCGCTGCTGGACGCCCTGGCGTATTGCTGGTGCCTGGTGCAGGCC  
CTGGTTGCCGAAGGCGCGTTGCCCTGGCGTGGCTGCGCTGGCTTGAGCCTGGCGCAG  
GCGCTGTTGCAGTACCTGCCCTGCGCTGCCGGTTTCGCCGCCGGCGCTCGCTGGCGGCTGGACTGG  
TGCGCAGCCTGGTGGCGCCTGCCGCCCTGGCGCGGCCGGCTGCGCCGGTGC  
AGGCCTGCTGCCGGCCGGTGAATGCAAGGCATGGGCATTCCGGCGCACCTGCTGGGGCCGCTGATC  
GCCCGCTGGTGACGCCGCTCGGGTGATCCTCGGGCTGTTCTGATCGACCCGTC  
GCCCTGCTCTGGCTGGGCCCTCGCCGCGCTGTTGCCTGGAGCGGGCGGCCAATCTGGCGGC  
GGAGGATGCCCGCTGGCGGCCGAGCGCGACGCCGACGGCAGTTGCAGGGCTCGCCGAACGCCAG  
CCACTGCTGCCGCCGCCAGCGCGAACAGCGTCGCCGCCAGGGGCTGGAAGAGGCC  
TCCACCGCAGCACCTGGATCTGTTGCCGCCAGGCCAGCGGCCCTGCCCTGGCG  
GCAGGGCGCTGCCCTGCCCTGCTGCCGCCCTGGCGCTGGCTGGGCCAG  
GCTCGGCTGGTGGCGCTGCTGGTGCCTGCTGGCGCTGGCGCTGGCTGGACGCC

```

TCGACCAGGCCTTGCAGGGCGCTGGCAGGGCCTGGATACCCCTGCTGCGGGTTTCGCCCTGGCTCC
GCTGCGCAGCCCCGAGCCGGCGAGCGGCCACGACGCCAGCCTGGCGGCCAGGGCGTGGAAATTG
CGCTGGAAAGATGGCCGGCCCTGCTCGAGGACATTCCCTGAGGCTGGAGCAGGGCTGGCTGCTGACCG
TCCTCGTGGACCCCTCGGGGCCGGAAGAGCAGCCTGCTGGCGCTGCTGGCGCTACGACGT
CGATGCCGGCGTGTCTGCTGGGTGGCGTGGATATCCGCCGGTTAGCGAAACGACCCCTGCCGCC
AGTCGTAACCTGGTGTTCAGGACAAAGCCCTGTTCCGCCAGCGTTGCCCTGGAACCTGCGCATGG
CCCGAGCGGACGCCGATCTCGAAGCGCTGCGAGGCAGGGCGCTGGCGAGGCGGGTTGGCCTGCTGGAAGAGAT
CGAGGGCCTGGCGCAGGGCTGGGACAGCGACGTCGCTCCGGCGCGCTGCTGTCGGCGGCCAG
CGGCAACGCCTGTGCCTGGCTCGCAGGGCGCAGGTGCTGCCAGGCTGCTCGCTCGACGAGCCA
CCGCCAGCCTCGACGCCAGCGAGGCGCAGGTGCTGCCAGGCTGCTCGCTCGGTTGCCGGCGGCCAG
CACCTGCTGGTAGTGAACCAACCGCCGGCGCTGGCGCAGGCCGACCAGGTACTGCTGCTGGAG
GAGGGCGCCTGCGCCTAGCGGACTTCACGCCGATCTGCTCGTCCGGACGACTGGTATGCCGGTT
TCGTCGGGCTGGCGGGGAGGAAAGTCCCGACGGTCGTGGATCGATAG

```

The VIR18 protein (SEQ ID NO:36) encoded by SEQ ID NO:37 is presented using the one-letter amino acid code in Table 20B.

**Table 20B. Encoded VIR18 protein sequence (SEQ ID NO:36)**

```

MTLFERMALPEDCRAALRRASAWAVLAALLDAACGVLLVPLVEAWFAEGLPWRWVAALLGLSL
AQALLQYLALRRGFAAGGSLAAGLVRSLVRLPRLAPPALRRVAPAEGLLRGPMQAMGIPAHLL
GPLIAALVTPLGVLILGLFLIDPSIALGLLLAGAFLAALLRWSGRRNLAEDARLAAERDAARQLO
AFAERQPLLRRAAQRESVARQGLEEALRSIHLRSTLDLRLRSLPGLFALAVQAAFAALLGGAWA
VERQWLDGARLVAVLVLLVRFIEPLAQLTHLDQALRGAWQALDTLLRVPFALAPLRSPEPGERPHD
ASLAAEAVEVLRLEDGRALLEDISRLLEPGSLNVLVPGSGACKSLLALLGRLYDVDAGRVLGGV
DIRRLSETTLAASRNLVFQDNGLFRGSVAWLRMARADADLEALREAARAVGLLEEIEAWPQGWD
SDVPGGGALLSGGQRQLCLARGLLSTAPLLLDEPTASLDAASEAQVLRSLLGI,RGRRTLLVVT
HRPALARQADQVLLLEEGRLRLSGLHADLLVRDDWYAGFVGLAGEESSATVVDR

```

5

The role of VIR18 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

### MUT19

10 A *Pseudomonas* bacterial mutant (MUT19) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as a gene cluster encoding the *P. aeruginosa* serotype 09 putative O-antigen biosynthesis pathway

15 (VIR19). The insertion site nucleic acid sequence identifying the VIR19 gene in MUT19 is shown in Table 21.

**Table 21. MUT19 Transposon Insertion Site (SEQ ID NO:37)**

```

CTCTTTCAGCCGCACGCCGGCGCACCTCGTGTGATCAGTGAGTGGTTGCAACTGCAGGGTCAAG
GATCTGGATTCCCTCACANGTNCGATCATCGTGCAGGGAGGGCAAGGGCTCAAGGATCGGGCCT
TGATGTTACCGAGAGCTGGCACCCAGCCTGCCGAGCAGGGNNAAATTGATCCGGTGGATGACC

```

```

TTTGAAATGACCTTAATAGATTATTAATTACTAATTAAATTGGGACCTANAGGTCCCCCTTTTTA
TTTAAAAATTTCACAAACGGTTATTNCATAAGCTTGCCTAATCAATCACNTATCCN
CGGAATTGGCCTAGGCGGCCAGATCTGATCAAGAGACAGACTCCAGCTTGCATCCGGAGCG
ACCACACGAGCAGGTCACTTCACTGAAGGAATTCTGACATAGATCTCACCAACCTTC
CATGTCCTCAAAGGCATGCCACACTAATCGACGCCCTCCTCAAAGAAATCATGAACCGGGTCA
TCCGCTCATCAGTGATAGGCAAGACGCCCTGTCCTG

```

The role of this cluster in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

5

#### B. Attenuated *Klebsiella* Mutants

##### MUT20

A *Klebsiella* bacterial mutant (MUT20) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a hypothetical transcriptional regulator in met G-dld intergenic region (VIR20). The insertion site nucleic acid sequence identifying the VIR20 gene in MUT20 is shown in Table 22.

15

**Table 22. MUT20 Transposon Insertion Site (SEQ ID NO:38)**

```

ACGCAGGATATCTCTTCATCAAATTGTCGATGCCGCCCTCGCTACGCTGCAGTTCACTAGACCG
TAACGACGCTGCCAGGCGCGCAGTGTGACCGGATTGATTCCGCAACGTTCGGCCACTTCACCGATAC
TGTAAAACGCCATAGCGCCCTCACATCAACCTGATACCTTAATACCTAAACTAACGAATTCAAGGCAT
CCTGTACAACCTATTTCTTGTACAGATAAGATATCAGGTTGCGGCTCACAGCGCCGGAAAAAA
AGATGAAAAAAATGTTAGCTGATTTCGCGGTGGTCATTTCCTCCGGCATGCGACGGGGTAG
GCCCGCCAGGCGCGCTGGCGAACAAATTGCCCTGAAACTGTGAAATACCGGCTGATTCCAGCCAC
ATCCACTCTCAGCACGCTCAACGCCGACGGCTGAGACCGCAATCTCAGAGAAGTACAGCATTGA
TAATCGCTG

```

##### MUT21

A *Klebsiella* bacterial mutant (MUT21) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding  $\alpha$ -cystathionase (VIR21). The insertion site nucleic acid sequence identifying the VIR21 gene in MUT21 is shown in Table 23.

**Table 23. MUT21 Transposon Insertion Site (SEQ ID NO:39)**

```

GACCATGTGCTGATGACCAATAACGCCCTATGAGCAAGCCAGGACTTTGTACCAAAATTCTGCCA
AACTCGGCGTCACCACCAAGCTGGTCGATCCCTTAATCGGCGCCGATATCGCCCGTCTGGTTGCC
TGAGACCCGCGTGGTCTCGAATGCCCGCTCGATCACCATGGAAGTGACGATGTGCCGGCG
ATAGTCGCCGCCGTGCGTCAGGTGCCCGGAAGCGATTATCATGATCGATAACACCTGGCGGCG
GGATCCCTGTTAAAGCCCTGGATTGGCATTGATATTCCATTAGGCAGGCAACAAATACCTGAT
CGGCCATTCCGACGCCATGGTGGCACCGCGGTGGCAACGCCGCGTCTGGCCGCAGCTGCGTGA
AATGCCCTACCTGATGGGCAAATGCTGGACGCCGATACTGCCTATATGACCAGCCGCGGCTGCGA
CCCTGGCGTGCCTGCGTCAGCATGAAAGCAGCCTGCGCATC

```

**MUT22**

A *Klebsiella* bacterial mutant (MUT22) was made by transposon insertion in a 5 *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as ribosome binding factor A (VIR22). The insertion site nucleic acid sequence identifying the VIR22 gene in MUT22 is shown in Table 24.

10

**Table 24. MUT22 Transposon Insertion Site (SEQ ID NO:40)**

```

CTTTGGCCCTTTTGTCTTATTCTGGAGAACTTATATGGCAAAGAATTGGTCGCCCGCAG
CGTGTGGCCCAGGAGATGCAAAAAGAGATTGCCATCATCTGCAGCGTGAAATTAAAGATCCGCGTC
TGGGCATGATGACCACCCTTCCGGTGTGAAATGTCCTGACCTGGCTATGCCAAGGTGTATGT
CACCTTCCTAACGACAAGATGAAGCCGCGGTGAAAGCGGGCATCAAAGCGCTGCAGGAAGCTTCT
GGCTTATCCGCTCTGCTGGGAAAGCGATGCGTCTGCGCATCGTACCGGAACTGACTTTCTCT
ACGACAACACTGTTGGAAAGGGATGCGTATGCCAACCTGG

```

**MUT23**

A *Klebsiella* bacterial mutant (MUT23) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding aspartokinase/homoserine dehydrogenase (VIR23). The insertion site nucleic acid sequence identifying the VIR23 gene in MUT23 is shown in Table 25.

**Table 25. MUT23 Transposon Insertion Site (SEQ ID NO:41)**

```

GCCAGCCCGCTTCCGCTTGGCCAGTTAAAGCCTCCGGAGCAGGAATTGCTCAGATTAAGC
ATGTCCTGCACGGCATCAGCCTGCTGGTCAGTGCCGGACAGCGTCAATGCCGCGTGTATCTGCCG
CGCGAAAAGCTCCATGCCATCATGGCGGTCTGCTGGAAAGCCCGTGGACACAAAGTCAGTGTGTC
ATTAACCCGGTCGAAAATGCTGCCGTGGTCAGTATCTGGAATCCACCGTCGATATGCCGAAT

```

```

CCACCCGCCGCATTGCCGCCAGCCAGATCCCGGAGACCATATGATCCTGATGGCCGGGTTACCGC
CGGCAATGAGAAAGGCAGCTGGTGGTGTGGCGTAACGGCTCGACTACTCGGCTCGGTACTG
GCCGCGCTGCCCTGCGCGCTGACTGCTGCGAAATCTGGACCGATGTCGACGGAGGTGACACCTGCGATC
CGCGTCAGGTGCCGGATGCGCGCTGCTGAAATCGATGTCCTATCAGGAGGGATGGAGCTCTCCTA
CTTGCGCGAAAGTGTGCAACCGCGCACCATTGCCCTATGCCAGTTCCAATCCCATGCCCTG
ATTAAAAATACCGGCAACCCCC

```

## MUT24

A *Klebsiella* bacterial mutant (MUT24) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding cystathione • -synthetase (VIR24). The insertion site nucleic acid sequence identifying the VIR24 gene in MUT24 is shown in Table 26.

**Table 26. MUT24 Transposon Insertion Site (SEQ ID NO:42)**

```

GGCGCAGCGCTGCTCGTCACCGTCAGCTCGAAGCTTAACATTGCCAAAACCTTTGCTGACG
CGCCGCAATTTCATGCCCTGGTTTCCGGCAGCGATGGATGATACAGCTTTCACAGCGGCTGG
GTTTCAGATACTCAACGATCGCCAGGGATTGCTGCTGCCACTTCCATCCGGAGACAGCGTCC
GCAGCCCGCGAACAGCAGATAGCTGCGAAGGCCTGCCGGTGACGCCAATTATTACGCCACCA
TGCCAGTTCGGTGACAGTTGCCGGATTTGCAATCACCACCCGGCACACATGGAGTGACCA
TTGAGGTATTGGTACAGGA

```

10

## MUT25

A *Klebsiella* bacterial mutant (MUT25) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding phosphoribosylformylglycinamide synthase (VIR25). The insertion site nucleic acid sequence identifying the VIR25 gene in MUT25 is shown in Table 27.

**Table 27. MUT25 Transposon Insertion Site (SEQ ID NO:43)**

```

GTTGCGTCCCAGGGGGTAAACGCATCCTGCAGGTAGTCATTGTCGTCGGCCAGCGCCAGACCC
AGACGGAGGTGGCGTCAATCAGCGCCTGACGCCCTCGCCCGAGCAGGTCGACGCTGGTGACCGGCG
TCGGCTGATGGTGAGCGAACAGCTTCTGCCCGCTTCCAGCTCGTCAAGACGCTCTCCATCATGCG
GTCATGCAGCTCCGCCGCACCGCGCCACTGCGCTCGTCAGGGTTGAGGCTCAACGTAATAAC
GCCACGCCGCCCTCAAGACGCACAAACCTGCGCAGACCGCAGTTGTGAGCGATATCGGTAGCTTAG
AAGACCAAGGGAGAGATGGTGCCAGGGCGAGGGGTACAGGAGCAGTAATTACCGGTGGGTATGGCT
GCTTAAGCTGGGCCATACTGAAGCAGTCGCCAGCGCTCGCAGTCGTCAGCGCTCAGCGGGCG
TTCAGATCGGCAAAATGAATATATTCCGGCAT

```

**MUT26**

A *Klebsiella* bacterial mutant (MUT26) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding homoserine transsuccinylase (VIR26). The insertion site nucleic acid sequence identifying the VIR26 gene in MUT26 is shown in Table 28.

**Table 28. MUT26 Transposon Insertion Site (SEQ ID NO:44)**

```
GTATTGGCATCGTACTCCTGGGCTGGCGGTGACAAAGGCATGCCCTATCTTGCTGGCGAACAA
ATACGCATCGCCCTCTCCGCTCCCGAGGATCTGAGATCGGTATAGTCGCAATAAGTCCGGCC
GGAAAATCAGCATAGCGTGAGTGCGGGGCCAGGAAGAGTCGTCGAAACCGCGGGTCAGTAAGGC
GCGGATGAAGAATATGGTGTTCATAGACGCCGAAATCTTTCGGCGGGCTGCTTGGGAATGCC
GTACAGAATGTTCAAGCGGGCCTGAACCGCCCAACAGACGAACAGCGTCGAAGTGACGTGATCCTG
GCCCACTCCAGCACCTGTTGATCTCGGCCAGTAAGAACATCGTTAAACTCAACCAGGCCTAAAG
GAGCGCCGGTAACAATCAGGCCGTCAAAGTTCTGATC
```

**10 MUT27**

A *Klebsiella* bacterial mutant (MUT27) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 3'-phosphoadenosine 5'-phosphosulfate reductase (VIR27). The insertion site nucleic acid sequence identifying the VIR27 gene in MUT27 is shown in Table 29.

**Table 29. MUT27 Transposon Insertion Site (SEQ ID NO:45)**

```
GAGGTTCATATGTCCGTACTCGATCTAACCGCGTTAATGCATTGCCGAAAGTGGAACGCATTCTGG
CACTCGCGAAACCAACGCCAACCTGGAAAAGCTTGACGCCGAAGGGCGTGTGGCGTGGCGCTGG
AAATCTGCCGGAAACTATGTGCTGCGAGCTTGGCATTCAAGGCCGGTAAGTTGCATCTG
GTGAATCAGATCCGCCGGACATTCCGGTATCCTCACCGATAACCGCTACCTGTTCCCGAAACCT
ATCAGTTATTGACGAGCTGACGGACAAG
```

**MUT28**

20 A *Klebsiella* bacterial mutant (MUT28) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the

gene encoding Sfi protein (VIR28). The insertion site nucleic acid sequence identifying the VIR28 gene in MUT28 is shown in Table 30.

**Table 30. MUT28 Transposon Insertion Site (SEQ ID NO:46)**

```
TGTTAAAGCGTGCCTCTACAGCCTGTTAGCCTGCTCGGCCTGCTGCTGTTGACCGTGCTGGGCCT
TGACCGCTGGATGAGCTGGAAAACCGGCCCTATATCTATGATGAACTGCAGGACCTGCCCTACCGT
CAGGTCGGTGTGGTGTGGCACCAGGCAAATATTACCGCACCGGCGTCATCAATCAGTATTACCGTT
ACCGCATCCAGGGTGCCTGAACGCTACAACAGCGGCAAGGTCAACTATCTCTGCTGAGCGGGGA
TAATGCTCTGCAAAGCTACAATGAACCGATGACCATGCGTCGGGACCTGATTAAAGGCGGGCTCGAT
CCCGGGATATCGTACTGGACTATGCCGGTTCCGTACCCCTGACTCGATCGTCCGTACCCGGAAAG
TGTCGACACCAACGACTTCATTATCATCACCCAGCGCTTCACTGCGAACGGCGCTGTTATCGC
CCTGCATATGGGATCCAGGCCAGTGCTACCG
```

## 5 MUT29

A *Klebsiella* bacterial mutant (MUT29) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the 10 gene encoding transcriptional activator protein LysR (VIR29). The insertion site nucleic acid sequence identifying the VIR29 gene in MUT29 is shown in Table 31.

**Table 31. MUT29 Transposon Insertion Site (SEQ ID NO:47)**

```
CGCTGAACCTCTCAAAACAAACGCAGGCCCTGCACCTGTCGGCTGCAGGCAGCGTGATCCGC
TCAAACAGCTGCAGGCCGAGCACCTCTCAAAGCGGCCAGCTCGCGGCTGACCGTGGGTTGCGAGG
TGTGCAGCATCCGCCGCTTCGGTCAGGTTGCCGGTGGTCATCACCGCGTAAAGATTTGATATG
ACCGAAATTGACGGCTGGCATCGGGCTCCGTGAGGCTCGGCTGGAACCATATCATTTTGCATAGA
GTCGGATAAAACGATATTTTATTCGTCTGTCACTGTGGCGTAATCAGAAAAAACAGCGACCAAC
ACACGCACTGCACCGGAGTTCTTATGCCACACTCGCTTACGCCACCGATACTGACCTGACCGCGGA
CAACCTGCTGCCCTGCCGGGAATTGGCTGCCGGTCTGGGTCTATGATGCGCAGATTATCGC
CGCCAGATAGCCCAGCTCAGCCAGTTCGAC
```

## MUT30

15 A *Klebsiella* bacterial mutant (MUT30) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding TrpD (VIR30). The insertion site nucleic acid sequence identifying the VIR30 20 gene in MUT30 is shown in Table 32.

**Table 32. MUT30 Transposon Insertion Site (SEQ ID NO:48)**

```
GGCTTCCACCCAATCGTTGCGCAACGATTTGCTAAAACGGCTTGCAATTCTTACCCCTCT
TGCCCGCTAAGTGCCTGCACTCTGTCATAGGCCGCCGCTGCTGCAGCACATCCAGTACCTGCTGA
GCGTTAGCTTCAGATCTCATGCCGTGAAACGCATCAATATGGCAGCTGGCGGCGACGGCGG
CTTCGTGAGCGGCTCACCTTACCTG
```

**MUT31**

A *Klebsiella* bacterial mutant (MUT31) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding N-acetylglucosamine-6-phosphate deacetylase (VIR31). The insertion site nucleic acid sequence identifying the VIR31 gene in MUT31 is shown in Table 33.

**Table 33. MUT31 Transposon Insertion Site (SEQ ID NO:49)**

```
TGGCTAACGCTGCTCAGTGGTGCAGGGTGTCACTTGGTATCACATCGCGTTGTCTGCACAGTG
AAATCAGATCCAGGCCCGCTCCGGTTTACGCACGTAGTCCGGATTGGGGTGCCTTCTTAACGA
TATTCAAGCCACGGCCCTTCGAGATGCAGGCCAGCGCCTGGTCGGATGTTTGCAGATATTGCG
CATCACGCGCACGCCCTGCTTCATCAGATCGCTGGAGGTAAATCAGCTGCGCAGGAAGCTGGTG
CAGCCTGAGCGTTCGTTGGCCTTCTGCATGATCTCCAGCGTTTCGACAGTGACCGCCTCTGGCTGT
CGTTAAACTGCACGCCGCCAGCCGTTGAGCTGGACGTCGATAAAACGGGGCGATTATTGCGCC
GTTGACTGAGCGCTGCTCGATGTCAGACGGAAATCTGCCAGCGGACAAAGACGTTCGATAAAAG
```

10

**MUT32**

A *Klebsiella* bacterial mutant (MUT32) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding WaaQ (VIR32; Regué *et al.* J. Bacteriol. 183(12): 3564-73, 2001). The insertion site nucleic acid sequence identifying the VIR32 gene in MUT32 is shown in Table 34.

**Table 34. MUT32 Transposon Insertion Site (SEQ ID NO:50)**

```
TTAACGCACCATATCGTACCGCTGCTGGCGCAGCGTCTGAATGAGCTGCCATTGCACTTCAGCTGAT
ACCTTTTCCCTGGCTTTCCAGCGCGATCGAGACCATAATATGGGGATATCGGGGTTGGCTG
CGAGCATATCCCGGGTCTTCATACAACAGGACATCCACGCTGGCGGGTACTGCTGTTCA
CGCGTGAATAAGCGCGTGATCAGCAGCATGTCGCCATGATGGCGCAGCTTAATGACCAGGATCCGC
GCCGGGTTCAACGGGCCGCCAGAGGGTTTCAGCGTCATACTCTGTTCTCATCCAGGATAAGGG
TTCCGATTCTAGGGGATCAGACAGATTGAGAGAAGCGTTGATGCTCTACCATGACCGATAACGTA
TGGCCTGAGGACGTTTCGTGCACAATCCCGCAATTCTCATCAGAT
```

**MUT33**

A *Klebsiella* bacterial mutant (MUT33) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 2-isopropylmalate synthase (VIR33). The insertion site nucleic acid sequence identifying the VIR33 gene in MUT33 is shown in Table 35.

**Table 35. MUT33 Transposon Insertion Site (SEQ ID NO:51)**

```

CACTCAGGCTTGCCGTAAACGCTTGGCCATCACGTAAGGCGTATCGAAAATAATGACTTGCTG
GCTCATGGTTGGATCCTAGTCTGTGCTGGCGCTTGTGACGAGCATAAAAAACCGCGGCCA
AGGGCGGGTTTATAGCTTGCTGGAAGATGACTTAACGCTGAACGTCGCCAACAGCCTACCGAG
CAAATGGCATGCGTTAGTAGTAGCTGGATACGAGCGGTGCGAATCATTGCGTCAAACCTCC
AGATGAAATCGTTATGCTTTAGAGTTACTGGATAGCCGTTAAAGTCAACCCCTGGCATGGAAA
AGCGTTTGGGCTGACTAAATGAATTAGCAAATGTCGATGTAAGCCCCATTGCGAAGATCC
TATTTGGACCGAAGGCGTTATCCCCAATTGTTCAATTGAAAAA

```

10

**MUT34**

A *Klebsiella* bacterial mutant (MUT34) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding histidinol dehydrogenase (VIR34). The insertion site nucleic acid sequence identifying the VIR34 gene in MUT34 is shown in Table 36.

**Table 36. MUT34 Transposon Insertion Site (SEQ ID NO:52)**

```

CGCTGAACCGCTATCCGGAGCCGCAGCCGAAGTGCCTGATTGAGAGCTACGCCCGCTACGCCGAGG
TCAAACCGGAGCAGGTGCTGGTCAGCCGCGGCCGACGAAGGCATCGAGCTGCTGATCCGCGCCTT
CTGTGAGCCCGCGAAGACGCGGTGCTACTGCCCCGCCACCTACGGCATGTACAGCGTCAGCGCC
GAGACCATCGCGTCGAGTGCCGCACCGTGGCAGCCTGGCAGCTGGCAGCTCGACCTGCCGGGCA
TCGAAGCGCGGTGGACGGCGTGAAGGTGGTGTGTTGCTGCAGCCCCAACACCCGACCGGGCAGAT
TATCGACCCGCAGTCGATGCGCAGCTGCTGGAGATGACCCGCGGAAAGCCATCGTGGTGGCCGAC
GAAGCCTATATTGAATTCTGCCGCAGGCGACGCTCGCCGGCTGGCTCAGCGACTATCCGACCTGG
TGGTGCTGCGCACGCTGTCAAAGCCTCGCCCTGCCGGCCTGCGCTGCGGCTTCACCCCTGCCAA
CGCCGAGGTGATTAACGTGCTGCTGAAAGTGAATCGCCCC

```

**MUT35**

A *Klebsiella* bacterial mutant (MUT35) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding UDP-galactopyranose mutase (VIR35; Clarke *et al.*, J. Bacteriol., 177: 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR35 gene in MUT35 is shown in Table 37.

**Table 37. MUT35 Transposon Insertion Site (SEQ ID NO:53)**

```
CGTATATTCATCGTACAGAACCGTAAACACAGGCATTGGCTGATTTCACTGAGTGAATTAAAT
AGACTTCTGCCGTTTCATGCTCGCGATGGTCACATCCATATCAAGGTACCGTAGGTTCCAAG
ACGACCGACAAAAGTGAATGTTGGTTTCATTCTCGGCCATGACAATATTTCAAGAAGAGCCATT
TCTCCCATCTGGCGAATAGGATAGTAAGGAATATCATTTCACAAGCACGGCTATACTCTTAT
AACAAACAGAGCCGTGTTGTTCCCAGGGAGAAAATATTATGTTCACTGAGTGCAGTATAGGG
CACATCCACAGAACAGTAGTTCATCACTGCGCATCCCTGG
```

10

**MUT36**

A *Klebsiella* bacterial mutant (MUT36) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding O-antigen export system permease protein rfba (VIR36; Bronner *et al.*, Mol. Microbiol., 14: 505-19, 1994). The insertion site nucleic acid sequence identifying the VIR36 gene in MUT36 is shown in Table 38.

**Table 38. MUT36 Transposon Insertion Site (SEQ ID NO:54)**

```
GTACGCCGATTTATATCGCTCTGATATGATTCCGGAAAAATTAGCTGGATAATTACCTACAATCC
GCTAGCGAGTATGATTCTAGTTGGCGTGAATTATTCAATGAAATGGGACTCTTAATTGGAGTATATT
TCTATACTCTATTTACGGGAATTATTTGACGGTTGTCGGTTGTCTATTTCATAAAATTAAAAT
ATCGATTTGCAGAGATCTAAAAGTGCCTATAAGAGCAGCATGCTAGGCTATTATGGTCAGTAGCA
AATCCATTGCTTTGCCATGATTACTATTATTTAAGCTGGTAATGAGAGTACAAATTCCAA
ATTATAACAGTTTCCTCATTACCGGCTTGTTCGGCAATGGTTGCCAGTCGGCCACTAAC
```

20

**MUT37**

A *Klebsiella* bacterial mutant (MUT37) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding uridyltransferase (VIR37). The insertion site nucleic acid sequence identifying the VIR37 gene in MUT37 is shown in Table 39.

5

**Table 39. MUT37 Transposon Insertion Site (SEQ ID NO:55)**

```
CGAGCCACCCACTGTAGCGTATGGATATCGCGCAAGCCGCCGGGGCTGCTTTCACGTCCGGCTCGA
GGTATAGCTGGTGCATGATAGCGCTGATGACGGACGTTCTGCTCTCGACCTTGGCGGCCGAAGAA
CTTTTCCGATGGCCAGAACGCCGCTGCTAAAAATATGTTTGCAAGGAAACAGCGCGACGTCG
CCGATCAGCAGGCGCGATTGATTAAGTTGGTGGCAACGGTCAGATCCGAGAGACCTTCAGCAGGC
ACTCTCGAGGGTGCCTACGCTGTGGCCACCTCCAGCTGACGTCCCACAGCAGGGTGAGCAGTTC
GCCGACTTTTGCCTGGTCGTCCGGCAGTTTACGACTGAGGATCAGCAGATCGACGTCTGAG
AGCGGGTGCAG
```

### MUT38

A *Klebsiella* bacterial mutant (MUT38) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

10 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyridoxine phosphate biosynthetic protein PdxJ-PdxA (VIR38). The insertion site nucleic acid sequence identifying the VIR38 gene in MUT38 is shown in Table 40.

**Table 40. MUT38 Transposon Insertion Site (SEQ ID NO:56)**

```
CTTAACCCGCACGCTGGCGAAGCCGCCATATGGAACAGAACAGAGATAGACACCATCATTCCGGTGC
TGGAAAGAGATGCGCGCAAAGGGGATGAACCTCAGCGGTCCGCTGCCGCAGACACTCTCTTCAGCC
GAAATATCTTGATCATGCGATGCGGTACTCGCGATGTACCGACGATCAGGGCCTGCCGTGCTAAAA
TACCAGGGCTTGGCCGGCGGTGAACATTACGCTCGGTTACCTTATTCTGACCTCCGTCGACC
ACGGCACCGCAGTGAATTAGCGGGCCAGGGAAAAGCGGACGTCGGCAGTTTATCACGGCGCTTAA
TCTCGCCATAAAATGATTGTTAATACCAATGAATAATCGAGTCCATCAGGGCATTAGCCCGCA
AACGCTCGGGCAGAACTCCCTCAACGATCAGTTGTGATCGACAGCATCGTCTGGCGATTAACCC
GCAGAAAGGCCAGGCGATGGTGAATCGGC
```

15

### MUT39

A *Klebsiella* bacterial mutant (MUT39) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

20 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding triose phosphate isomerase (VIR39). The insertion site nucleic acid sequence identifying the VIR39 gene in MUT39 is shown in Table 41.

**Table 41. MUT39 Transposon Insertion Site (SEQ ID NO:57)**

```

GGGTCTGACCCGGGTTCTGTGCATCGGTGAAACCGAAGCCGAAACCGAAGCGGGCAAAACCGAAGAA
GTTGCGCACGTCAGATCGACGCCGTGCTGAAAACCCAGGGCGTCCGCTTCGAAGGCCTGGTTA
TCGTTACGAACCACTGGCTATCGGTACCGCAAAATCAGCGACCCCGGCTCAGGCCAGGCGGT
GCACAAATTCCGTGACCACATTGCTAAAGCTGACGCCAAATCGCTGAGCAAGTGATCATCCAG
TACGGCGGTTCCGTTAACGCTGGCAACGCCAGAGCTGTTACCCAGCCGACATCGACGGCGC
TGGTTGGCGCGCCTCCCTGAAAGCTGACGCTTCGCGGTGATCGTTAAAGCAGCAGAAGCAGCGAA
AAAAGCGTAATTGCTTTCCCGGTGGCGACACGCGACCCGGTTGACTGACAAACGTGGAGCCG
GCCT

```

**MUT40**

A *Klebsiella* bacterial mutant (MUT40) was made by transposon insertion in a

5 *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding aldehyde dehydrogenase (VIR40). The insertion site nucleic acid sequence identifying the VIR40 gene in MUT40 is shown in Table 42.

10

**Table 42. MUT40 Transposon Insertion Site (SEQ ID NO:58)**

```

GGTGGCGCACCTGGCGTGTGTTGAGAAATTATGAATATTAATACCAGGAAATTCTTAATT
TGTGTACGCTCTGACGAGCGCACAAATAAAACAAGACGAATTGGAAACATTGCTTTAAATTGTT
AATTGAATTGATCTGTTGTTAAAGGTATTGAAATTCTTTGTATAGATATGTAATTAACAT
TGAAAGCCATTCAAAATTAAATATGGCGAACATAGCTATTAACTTATAGTTAACATCTCCC
GGGTGCGCTTGTGATACTCGGGTAATATATTATTTCGACATCAAATAACTCTTTCTCTG
TTTGTATTGATGCCATCTATTGGCGAAATAAGGCAGAGTAGAGGGGGATGTCGCTAATATCCTGC
GGAAGGAACGCAATGTACATTACAGGGAGGAGCTGACGAGCCGTTCGCGATAGCTTTAG

```

**MUT41**

A *Klebsiella* bacterial mutant (MUT41) was made by transposon insertion in a

15 *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding galacosyl transferase (VIR41; Clarke *et al.*, J. Bacteriol., 177 : 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR41 gene in MUT41 is shown in Table 43.

20

**Table 43. MUT41 Transposon Insertion Site (SEQ ID NO:59)**

```

TTGGTGGTGTGCTCGCGAAGAAATTAACTGCGCGTCATCGTAAGTTGTTGGCGTTGAAAGAGT

```

```

ATTTCTTCTGACAGCATGCCCTTAAATTATTGGCGCAGTTACTATTGCTGCATATAAATATATT
GCCAGTAATAAGCGCTGTATATTATGTTAACATGACCGCGACAGAAAAAAACTGGCTAAGTTGG
TTGGACTCGAAGAACAAACAGACTATTGTTATTGATGGTCAGGCATTAATCCAGAGATAACAAAATA
TTCTCTGAACAGGATCACGATGCCCTGTTGATTGTTGCCAGCGTATGTTGGAGTAAAGGA
CTGGCGACTTAATTGAAGCGAAGAAAATATTACGCAGTAAGAATATTCACTTACTTTGAATGTTG
CTGAATTCTGGTCGAAATGATAAAGATGCAATTCCCTCAGGGTATTGAAAATTGCGATCAGC
AAGGATTAATTAACTGGTTAGGTGTTGAATAATGTTGCGATCTATTGAGCAAT

```

## MUT42

A *Klebsiella* bacterial mutant (MUT42) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding siroheme synthetase (VIR42; Kolko *et al.*, J. Bacteriol., 183 : 328-35, 2001). The insertion site nucleic acid sequence identifying the VIR42 gene in MUT42 is shown in Table 44.

10

**Table 44. MUT42 Transposon Insertion Site (SEQ ID NO:60)**

```

TTACTTCCCCCTTTGCCGAAGTAAACAAAGGCCGTGCTGGTATCGGCCGGCGAGATTGCT
GAACGTAAGATCAAGTTCCTGCTGGCGCCCAGGCAGGTGCAGGTGGTCGCTGAAACGCTGTCAC
CGGCCTGGCCGATCTGGCTGGCGCCAGGCACACTCAGCTGGCGGGGAGCAGGCATTCAAGCAGACTCGCT
GGTGGATGATGTCTTCTGGTGAATTGGCAACCGAGGATGAGGCCTTAACCAGCGGGTGTGCG
GCAGCTAACGCGCGCTACCGGTTGGTCAACGTGGTGGATAACCAGGCCTGTGCTCGTTGTTCC
CTTCTATCGTCGACCGTTCGCCGCTGCTGGTGGCGATCTCCTCCAGCGGTAAAGCGCCGGTGTGTC
GCGCATTCTCGCGTGAAGGAAATCGAACGCGCTGCTGCCGACGAATCTCGGTGGCTGGCGGAATCAGCA
AGCT

```

## MUT43

A *Klebsiella* bacterial mutant (MUT43) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (VIR43). The insertion site nucleic acid sequence identifying the VIR43 gene in MUT43 is shown in Table 45.

20

**Table 45. MUT43 Transposon Insertion Site (SEQ ID NO:61)**

```

AGCAGGGCAATGGTGGCGGTTCTATAACATTCCCTGATGATGAAAGTCATATAACCGGCATTCTA
ACAGCAGCATTCAAGAGGGCAATGATTGGCAACCGATTACGACGATGCCGCAAATGCTAAAAAA
AGGGAGAGGGATTACCAGCTGGCGGGCTTTCCCGGCCAGATTATCCAGCACGGCGCAGCGCC
AGGCCGTCAAGGAAAGTGAAGGTCCGGCGATCTCGAACAGCGGCCAGAGCATAAAAGCCGGTTT

```

TCATATCGTAGTGCAGGAAACGGTCAGGCCTCGCTGTTAATGACAGCATCGCCAAACAGCATGATATC GAGGTCCAGCGTGCAGGCCCCCAGCGTTGCGACTCGCCCTGCTGCAGTCGATGCC TGAGTATGATCGAGCAGCGTCTCGGGGGCAGGGCGTTCCAGCGCAA
---

### MUT44

A *Klebsiella* bacterial mutant (MUT44) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding glucose-6-phosphate isomerase (VIR44). The insertion site nucleic acid sequence identifying the VIR44 gene in MUT44 is shown in Table 46.

**Table 46. MUT44 Transposon Insertion Site (SEQ ID NO:62)**

GGCTTAACGCCAGCTATGTCACCGCTGCAGGTTATGCGGATTTCATGCCTCTGCGGCTAACAGAAA AAAGCCTTATGATAGCTATACTAATGGGCTTTACTCCGTTTGACCCGATTCCTGACCAGCGTC AGGGTCAAGTCACAAAATCATCACAATTTCGTCACCGCGCTACAATCGACCGAAGTCACAATC TCAAATCAGAAGAGTATTGCTATGAAAAACATCAACCCAACCGAGACCTCTGCCCTGGCAGGCATTA CAGAAACACTTCGACGAAATGAAAGATGTCACTATCAGCGAGCTTCGCCAAAGATAGCGACCGTT TTCTAAATTTCGCGACGTTGCGATCTGATGCTGGACTTCACCAAAACCGCATCACTGAA AGAGACGCTGGCTAAACTGCAGGATCTGGCGAAAGAGACTGACCTGGCGGGCCTATCAAGTCGATG TTCTCAGGTGAGAAGATCAACCGCACCGAAGACCGCGCGTACTGCACGTCGGCT
---

10

### MUT45

A *Klebsiella* bacterial mutant (MUT45) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding DNA methylase (VIR45). The insertion site nucleic acid sequence identifying the VIR45 gene in MUT45 is shown in Table 47.

**Table 47. MUT45 Transposon Insertion Site (SEQ ID NO:63)**

TGCTTCATCCGCATCTCCTTGAAATTATTGGCTCTAGCCGACGGTAGAGCGCTAACATAGCTCGTC CACCTTTTACCGTACCAACCGTTGCTGCTGATGCTGCGCCGCACCTTCACAATATGCGTTCTGCC GCGTTTTATACCATTCTGCGTCAGCGCGTGCAGGTTGGAAATCAGCACCGGGATGCCCTTT TCATCAGCGATTCCGCCTTTGCGCCAGCAGTACCTGTTCCAGGTTGAAACTGTTGGTGGTA GGCGGTAAAGTTGCCGTCGCCGTTAGCGGCAGTACGGCGGATCGAATACACCAACTGTCGGCTA TCCGCACGTTGCATGCACTTCGTAAGATTGCAGTAAACTCGGCCTTGGCCCTTCAGCGCA AATGATAGAGCTCAGCTCGGGAAATAGGGCTTTATAACGGCAAACGGCACATTGAACCTCGCC GCGCAG
--

**MUT46**

A *Klebsiella* bacterial mutant (MUT46) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a putative inner membrane protein (VIR46). The insertion site nucleic acid sequence identifying the VIR46 gene in MUT46 is shown in Table 48.

**Table 48. MUT46 Transposon Insertion Site (SEQ ID NO:64)**

```
TGTC AAT GCGCAATTG GTTAAATATGCGGTATTGGCTGCTGGT GATGGGGCTTGCCGCCTGCGA
TAACAGCGATTCAAAGCGCCAACCGTTGGCGCAGCAGCGGAGAGCAATGCCAGCGGCCAGGCAATC
AGCCTGCTGGATGGCAAGCTGAGCTTCACCCCTGCCCTGCCGACCAAGAGCGGCAAAC TGG
GTACCCAGGCCAACATATGCACGTCTACTCTGACGCTACCGGCCAGAAAGCGGTATCGTCATCGT
CGCGACAGCACCAATGA
```

**10 IV. SUITABLE TARGET PATHOGENS**

Other *Pseudomonas* sp. and *Klebsiella* sp. and many other microbes, including gram-negative bacterial strains, are likely to include virulence genes encoding VIRX-related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Suitable bacterial pathogens may include, but are not limited to, *Pneumococci* sp.,

**15** *Klebsiella*, sp., *Pseudomonas*, e.g., *P. aeruginosa*, *Salmonella*, e.g., *Salmonella typhimurium*, *Legionella*, e.g., *Legionella pneumophila*, *Escherichia*, e.g., *Escherichia coli*, *Listeria*, e.g., *Listeria monocytogenes*, *Staphylococcus*, e.g., *Staphylococcus aureus*, *Streptococci* sp., *Vibrio*, e.g., *Vibrio cholerae*. Pathogenic mycobacteria of the present invention may include e.g., *Mycobacterium tuberculosis*. Pathogenic fungi of the present invention may include, e.g., *Candida albicans*. Pathogenic unicellular eukaryotic organisms of the present invention may include, e.g., *Leishmania donovani*.

Having identified VIRX genes according to the invention, it is possible to use the gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, e.g., EMBL or GenBank. The levels of identity between gene sequences and levels of identity or similarity between, amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the

BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 40% similarity with the peptides identified herein. More preferably, the 5 peptides have greater than 60% sequence similarity. Most preferably, the peptides have greater than 80% sequence similarity, *e.g.*, 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention may have greater than 40% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 60% sequence identity. 10 Most preferably, the polynucleotide sequences have greater than 80% sequence identity, *e.g.*, 95% identity.

In addition to related molecules from other microorganisms, the invention encompasses modifications made to the peptides and polynucleotides identified herein which do not significantly alter the biological function. It will be apparent to the artisan that the 15 degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptides. Complementary polynucleotides are also within the invention. Conservative replacements at the amino acid level are also envisaged, *i.e.*, different acidic or basic amino acids may be substituted without substantial loss of function.

20 It is recognized in the art that highly refined mechanisms that regulate transcription have evolved and are present in bacteria. Most bacterial genes are organized into operons, which are groups of genes coding for related proteins. Operons can either be repressed or induced thus regulating those genes. An operon consists of an operator, promoter, regulator, and structural genes. The regulator gene codes for a repressor protein that binds to the 25 operator, obstructing the promoter (thus, transcription) of the structural genes. The regulator does not have to be adjacent to other genes in the operon. If the repressor protein is removed, transcription may occur.

Transposon mutagenesis usually inactivates the gene in which the transposon is inserted, as well as any gene downstream in the same operon. If the VIRX gene is a structural 30 gene in an operon, inactivation of the VIRX gene disrupts the expression of other structural genes in the same operon and positioned downstream of the inactivated VIRX gene. For example, an insertion in pchE gene also inactivates pchF, pchG, pchH, and pchI genes

because they all reside within the pchEFGHI operon and are downstream of the inactivated pchE gene. Accordingly, the present invention includes attenuation of virulence due to alteration of a VIRX gene residing in an operon as well as alterations to nucleic acid yielding loss of expression of structural genes located in the same operon and located downstream of the VIRX gene. In one embodiment, the present invention is an alteration inactivating the first gene of an operon carrying a VIRX gene of the invention. The alteration of nucleic acids of VIRX genes and VIRX-containing operons may be insertional inactivation or gene deletion. It is preferred that the alteration of nucleic acids of VIRX genes and VIRX-containing operons be insertional inactivation.

The present invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation. In another embodiment, the attenuated bacterial strain has more than one mutation of an operon containing a VIRX gene when compared to an isogenic bacterial strain.

## V. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO IDENTIFY ANTIMICROBIAL DRUGS

### 25 A. Screening

In a separate embodiment, the VIRX genes, or their polynucleotide or polypeptide products disclosed herein is used in screening assays for the identification of potential antimicrobial drugs. Routine screening assays are known to those skilled in the art, and can be adapted using the VIRX products of the invention in the appropriate way. For example, the products of the invention can be used as the target for a potential drug, with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity. In the

methods of the present invention, one or more test compounds may be present or produced in the assay mixture. Preferably one compound is present, or produced, in the assay mixture.

#### **B. Character of Antimicrobial Candidate Compositions**

5       VIRX nucleic acids and polypeptides may be used to identify drugs or therapeutics in a candidate composition useful in the prevention or treatment of pathogen-associated disease or infection. A candidate composition can include one or more molecules for analysis in a screening assay and can be a synthetic or semi-synthetic molecules. Such molecules include inorganic as well as organic chemical molecules. The molecules may be less than about 500  
10      Daltons or more than 500 Daltons. The molecules may be naturally occurring. Naturally occurring molecules may include, *e.g.*, saccharides, lipids, peptides, proteins, nucleic acids, or combinations thereof, *e.g.*, aminoglycosides, glycolipids, lipopolysaccharides, or macrolides. Proteins may be immunoglobulins, *e.g.*, polyclonal or monoclonal antibodies. Nucleic acids may be DNA or RNA, *e.g.*, small interfering RNA (siRNA). The precise source of the  
15      molecule is not critical to the method of the present invention. The molecule might be derived from *e.g.*, synthetic compounds libraries that are commercially available, *e.g.*, Sigma-Aldrich (Milwaukee, WI), or libraries of natural occurring molecules in the form of bacterial, fungal, plant, and animal extracts such as those available from Xenova (Slough, UK). The synthetic (or semi-synthetic) or natural occurring molecules might be modified using standard  
20      chemical, physical, or biochemical methods known in the art.

#### **VI. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO DETECT THE DEGREE OF VIRULENCE OF PATHOGENS**

25      A diagnostic test can assist physicians in determining the type of disease and appropriate associated therapy. As such, a separate embodiment of this invention provides for the use of VIRX genes or their polynucleotides or nucleic acid products as virulence markers for detecting the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. There are many diagnostic assay approaches known to the artisan. Generally, the diagnostic method used would comprise the steps of (a) obtaining a sample  
30      from a potentially diseased subject or a diseased subject; (b) measuring the level of at least one polypeptide or polynucleotide virulence marker in the sample; and (c) comparing the amount of the virulence marker in the sample of step (a) to the amount of the virulence

marker present in a control sample from a second subject known not to have the presence of the pathogen, where an alteration in the expression level of the virulence marker in the first subject as compared to the control sample indicates the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. Preferably, the subject is a mammal. More preferred is that the subject is a human. The person of skill will recognize that diagnostic tests may be performed in an array-type format wherein, *e.g.*, the presence of two or more VIRX genes or gene products indicate the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen.

10 **VII. ATTENUATED ORGANISMS OF THE PRESENT INVENTION CAN BE USED IN VACCINE PREPARATION**

In another embodiment, the invention provides for the use of the attenuated organisms described herein in vaccine preparation. The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated 15 with suitable carriers or adjuvants, *e.g.*, alum, as necessary or desired, to provide effective immunization against infection. The preparation of vaccine formulations will be apparent to the artisan. The attenuated microorganisms may be prepared with a mutation that disrupts the expression of any of the VIRX genes identified herein. The artisan will be aware of methods for disrupting expression of particular VIRX genes. Techniques that may be used include, but 20 are not limited to, insertional inactivation, or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a second gene identified herein or in a separate gene required for growth of the microorganism, *e.g.*, an *Aro* mutation. Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or 25 nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be carried out by conventional techniques, including the use of recombinant constructs, *e.g.*, vectors, which comprise polynucleotides that express the heterologous antigen or therapeutic 30 protein, and also include suitable promoter sequences. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and the endogenous promoters used to control expression. In the vaccines of the present invention, the pharmaceutically effective dosage of the mutants of the present invention to be

administered may vary depending on the age, weight and sex of the subject, and the mode of administration. The subject can be, *e.g.*, a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

## 5    VIII. DEFINITIONS

As used herein, each of the following terms has the meaning associated with it in this section.

The term "pathogen," as used herein, is intended to include an agent that causes disease, especially a living microorganism such as a bacterium or fungus. The terms "agent" and "factor" are used interchangeably herein to describe pathogens or toxins useful in the methods of the present invention. Pathogens may include any bacteria, mycobacteria, fungi and unicellular eukaryotic organism, including wild types and mutants thereof, which causes disease or brings about damage or harm to a host organism. Pathogens may also be a poisonous substance, *e.g.*, toxin, which is produced by living cells or organisms and is capable of causing disease when introduced to a host.

The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism.

The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism.

The term, "virulence," as used herein, is a measure of the degree of pathogenicity of an agent to a host organism. Virulence is usually expressed as the dose of an agent or cell number of a pathogen that will elicit a pathological response in the host organism within a given time period. "Reducing the virulence" as used herein is defined as the ability of a compound to attenuate, diminish, decrease, suppress, or arrest the development of, or the progression of disease, damage or harm to a host organism mediated by a pathogen.

The term, "host organism," as used herein, is intended to include any living organism. Preferably the host organism is a eukaryote, *e.g.*, vertebrate. More preferably the host organism is a mammal. It is most preferred that the host organism be a human.

The term, "mutant," as used herein, an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype.

The term, "mutation," as used herein, is an alteration of one or more nucleic acids of a polynucleotide sequence encoding a gene. A mutation may include the insertion of additional nucleic acids to a polynucleotide sequence encoding a gene, e.g., insertional inactivation of a gene. Alternatively, a mutation may include, but is not limited to, deletion of one or more

5 nucleic acids of a polynucleotide sequence encoding a gene.

The term, "operon," as used herein, is a unit of bacterial gene expression and regulation comprising several genes usually with complementary functions. Typically an operon includes nucleic acid and control elements in the nucleic acid that may be recognized by regulators of gene products. Insertion in a gene in an operon interferes with the function

10 of this gene and of other genes located downstream or upstream in the operon. It is understood herein that the function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon.

The term, "pharmaceutically effective dosage," as used herein, means that amount necessary at least partly to attain the desired effect, or to delay the onset of, inhibit the

15 progression of, or halt altogether, the onset or progression of the particular condition being treated.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity" refers to a comparison between amino acid sequences, and takes into account not only

20 identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

## EQUIVALENTS

25 From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that bacterial genes have been identified and assigned a new role in virulence. Further, these genes and their products are useful in the identification of antimicrobial agents, the diagnosis of pathogen-associated disease or infection as well as the preparation of vaccines. Although particular embodiments have been disclosed herein in

30 detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and

modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. For instance, the choice of the particular pathogen, or combination of pathogens selected for assay or vaccination, the test conditions used in diagnostic assays utilizing the pathogens of this invention, or the method of mutagenesis used 5 to derive the attenuated mutants is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein.

## EXAMPLES

This Example is provided for the purpose of illustration only and the invention should in no way be construed as being limited to these Example, but rather should be construed to 10 encompass any and all variations which become evident as a result of the teaching provided.

### EXAMPLE 1 STRAINS AND CULTURE CONDITIONS USED TO SCREEN FOR ATTENUATED VIURELENCE IN TEST BACTERIAL MUTANTS.

The *D. discoideum* wild-type strain DH1-10 used in these studies is a subclone of DH1 (Cornillon *et al.*, J. Biol. Chem., 275(44):34287-92, 2000). Cells were grown at 21°C in 15 HL5 medium (14.3 g/l peptone (Oxoid), 7.15 g/l yeast extract, 18g/l maltose, 0.64 g/l Na<sub>2</sub>HPO<sub>4</sub>·2H<sub>2</sub>O, 0.49 g/l KH<sub>2</sub>PO<sub>4</sub>, pH 6.7) (Cornillon *et al.*, J. Cell. Sci., 107 (Pt 10):2691-704, 1994) and subcultured twice a week.

Bacteria were grown overnight at 37°C on Luria-Bertani (LB) agar. Single colonies were inoculated into 5 ml PB (2% (wt/vol) peptone, 0.3% (wt/vol) MgCl<sub>2</sub>·6H<sub>2</sub>O, 1% (wt/vol) 20 K<sub>2</sub>SO<sub>4</sub>) (Essar *et al.*, J. Bacteriol., 172(2):884-900,1990) in a 50 ml flask and grown at 37°C for 8 hr prior to use. The growth of various strains was tested in rich medium (PB) by measuring the optical density (600 nm) of a culture at different times after inoculation and was found to be comparable for all strains used. Under these conditions, similar OD<sub>600s</sub> were obtained for each strain and the induction of quorum sensing was maximal. Minimal 25 Inhibitory Concentrations (MICs) were determined in Mueller-Hinton broth by the microdilution method (Thornsberry *et al.*, NCCLS, 3: 48-56, 1983). Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced 30 virulence were identified and characterized by techniques well know in the art.

## CLAIMS

What is claimed is:

1. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

5 (i) a mutation of a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13,

VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23,

VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33,

VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43,

10 VIR44, VIR45, and VIR46; and

(ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

2. An attenuated bacterial mutant of claim 1, wherein said mutation is insertional inactivation or a gene deletion.

15 3. An attenuated bacterial mutant of claim 1, wherein said mutant is a gram-negative bacteria.

20 4. An attenuated bacterial mutant of claim 3, wherein said attenuated gram-negative bacterial mutant is a *Pseudomonas* species.

25 5. An attenuated bacterial mutant of claim 4, wherein said *Pseudomonas* species is *Pseudomonas aeruginosa*.

6. An attenuated *Pseudomonas* mutant of claim 5, wherein said attenuated *Pseudomonas* mutant is selected from the group consisting of: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19.

7. An attenuated bacterial mutant of claim 3, wherein said gram-negative bacterial mutant is a *Klebsiella* species.

5 8. An attenuated bacterial mutant of claim 7, wherein said *Klebsiella* species is *Klebsiella pneumoniae*.

10 9. An attenuated *Klebsiella* mutant of claim 8, wherein said attenuated *Klebsiella* mutant is selected from the group consisting of: MUT20; MUT21; MUT22; MUT23; MUT24; MUT25; MUT26; MUT27; MUT28; MUT29; MUT30; MUT31; MUT32; MUT33; MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43; MUT44; MUT45; and MUT46.

15 10. A method for identifying an antimicrobial drug, said method comprising:

(a) contacting a candidate composition with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46; and

(b) comparing the biological activity of said polypeptide in the presence and absence of said candidate composition, wherein alteration of the biological activity of said polypeptide indicates that said candidate composition is an antimicrobial drug.

25

11. A method of claim 10, wherein said candidate composition contains at least two molecules.

12. A method of claim 10, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

5 13. A method of claim 10, wherein said candidate composition contains at least one molecule greater than about 500 Daltons.

14. A method of claim 10, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

10

15 15. A composition of claim 14, wherein said polypeptide is an immunoglobulin.

16. A method for identifying an antimicrobial drug, said method comprising:

15 (a) contacting at a candidate composition with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and

20 (b) comparing the expression of said polynucleotide in the presence and absence of said candidate composition, wherein alteration of the expression of said nucleotide indicates that said candidate composition is an antimicrobial drug.

25 17. A method of claim 16, wherein said candidate composition contains at least two molecules.

18. A method of claim 16, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

19. A method of claim 16, wherein said candidate composition contains at least one molecule greater than about 500 Daltons.

5 20. A method of claim 16, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

10 21. A composition of claim 20, wherein said nucleic acid is a ribonucleic acid.

22. A nucleic acid of claim 21, wherein said nucleic acid is a small interfering ribonucleic acid.

15 23. A method for determining the degree of virulence of a pathogen in a subject, said method comprising:

20 (a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

25 (b) comparing the amount of said polypeptide in said sample of step (a) to the amount of said polypeptide present in a control sample from a second subject known not to have the presence of said pathogen, wherein an alteration in the expression level of said polypeptide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

24. A method of claim 23, wherein said subject is a mammal.

25. A mammalian subject of claim 24, wherein said mammalian subject is a human.

5 26. A method for determining the degree of virulence of a pathogen in a subject, said method comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, 10 VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

15 (b) comparing the amount of said polynucleotide in said sample of step (a) to the amount of said polynucleotide present in a control sample from a second subject known not to have the presence of said pathogen, wherein an alteration in the expression level of said polynucleotide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

27. A method of claim 26, wherein said subject is a mammal.

20

28. A mammalian subject of claim 27, wherein said mammalian subject is a human.

25 29. An attenuated bacterial mutant of claim 1, wherein said mutant encodes and expresses a foreign antigen.

30. An attenuated bacterial mutant of claim 1, wherein said mutant contains a plasmid which encodes and expresses, in a eukaryotic cell, a foreign antigen.

31. A vaccine against a disease caused by a pathogenic microorganism comprising:

- (a) a pharmaceutically effective dosage of one or more of the attenuated bacterial mutants of claim 1 and;
- 5 (b) a pharmaceutically acceptable diluent or carrier.

32. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

- 10 (i) a mutation of a gene selected from the group consisting of pchE, pchF, pchG, pchH, and pchI; and
- (ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

33. A bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein said bacterial strain includes a mutation that reduces expression 20 of said gene relative to an isogenic bacterial strain lacking said mutation.

34. A bacterial strain of claim 33, wherein said mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking said mutation.

09743PC.ST25.txt  
SEQUENCE LISTING

<110> University of Geneva  
<120> Virulence genes, proteins, and their use  
<130> 09743PC  
<150> US 10/324,967  
<151> 2002-12-20  
<160> 64  
<170> PatentIn version 3.1  
<210> 1  
<211> 1050  
<212> DNA  
<213> Pseudomonas aeruginosa  
<400> 1  
atggatatac aaggagccct caatcgcatc gtcaaccagc tcgacacctgac caccgaggaa 60  
atgcaggcgg tcatgcgcc a gatcatgacc gggcagtgca ccgacgcgca gatcggcgcc 120  
ttcctgtatgg gcatgcggat gaagagcgaa accatcgacg agatcgtcgg cgccgtggcg 180  
gtgatgcgcg aactggccga cggcgtgcag ttgcctacgc tgaagcatgt ggtcgacgtg 240  
gtcggcaccg gcggcgatgg cgcgaacatc ttcaacgtgt cctcggcgcc gtccttcgtg 300  
gtcgccgccc ctggcggcaa ggtcgccaaa cacggtaacc gcgccgtctc cggcaagagc 360  
ggcagcgcgcg acttgctgga agccgcccggc atctacctgg agctgacacctc cgaacaggtg 420  
gcgcgttgca tcgacaccgt cggcgtcggg ttcatgttgc cccaggtcca ccacaaggcg 480  
atgaagtacg ccgcccggtcc ggcgcgcgag ctgggcttgc ggactctgtt caacatgctt 540  
ggccccactga ccaacccggc gggagtcagg caccaggtgg tcgggggtt caccaggaa 600  
ctgtgcaagc cgctggctga agtgctcaag cgtctcggca gcgagcatgt gctgggtggtg 660  
cattcgccgcg acgggctgga cgagttcagt ctggccggcgg cgaccacat tgccgagttg 720  
aaggacggcgcg aggtacgcga gtacgaagtg cgtcccggagg acttcgggat caagagccag 780  
accctgtatgg ggctggaggt cgacagtccg caggcctcgc tggactgtat ccgcgcacgt 840  
ttggggcggc gcaagaccga ggctggcag aaggccggcgg agctgatcgt gatgaatgcc 900  
ggccccggcac tgtacgctgc cgatctggcg accagcctgc acgaggggcat tcaactggcc 960  
cacgatgccc tgcacaccgg gctggcacgg gagaagatgg acgaactggc ggccttcacc 1020  
gccgtttaca gagaggagaa cgcacagtga 1050  
<210> 2  
<211> 349  
<212> PRT  
<213> Pseudomonas aeruginosa  
<400> 2

## 09743PC.ST25.txt

Met Asp Ile Lys Gly Ala Leu Asn Arg Ile Val Asn Gln Leu Asp Leu  
1 5 10 15

Thr Thr Glu Glu Met Gln Ala Val Met Arg Gln Ile Met Thr Gly Gln  
20 25 30

Cys Thr Asp Ala Gln Ile Gly Ala Phe Leu Met Gly Met Arg Met Lys  
35 40 45

Ser Glu Thr Ile Asp Glu Ile Val Gly Ala Val Ala Val Met Arg Glu  
50 55 60

Leu Ala Asp Gly Val Gln Leu Pro Thr Leu Lys His Val Val Asp Val  
65 70 75 80

Val Gly Thr Gly Asp Gly Ala Asn Ile Phe Asn Val Ser Ser Ala  
85 90 95

Ala Ser Phe Val Val Ala Ala Gly Gly Lys Val Ala Lys His Gly  
100 105 110

Asn Arg Ala Val Ser Gly Lys Ser Gly Ser Ala Asp Leu Leu Glu Ala  
115 120 125

Ala Gly Ile Tyr Leu Glu Leu Thr Ser Glu Gln Val Ala Arg Cys Ile  
130 135 140

Asp Thr Val Gly Val Gly Phe Met Phe Ala Gln Val His His Lys Ala  
145 150 155 160

Met Lys Tyr Ala Ala Gly Pro Arg Arg Glu Leu Gly Leu Arg Thr Leu  
165 170 175

Phe Asn Met Leu Gly Pro Leu Thr Asn Pro Ala Gly Val Arg His Gln  
180 185 190

Val Val Gly Val Phe Thr Gln Glu Leu Cys Lys Pro Leu Ala Glu Val  
195 200 205

Leu Lys Arg Leu Gly Ser Glu His Val Leu Val Val His Ser Arg Asp  
210 215 220

Gly Leu Asp Glu Phe Ser Leu Ala Ala Thr His Ile Ala Glu Leu  
225 230 235 240

Lys Asp Gly Glu Val Arg Glu Tyr Glu Val Arg Pro Glu Asp Phe Gly  
245 250 255

## 09743PC.ST25.txt

Ile Lys Ser Gln Thr Leu Met Gly Leu Glu Val Asp Ser Pro Gln Ala  
 260 265 270

Ser Leu Glu Leu Ile Arg Asp Ala Leu Gly Arg Arg Lys Thr Glu Ala  
 275 280 285

Gly Gln Lys Ala Ala Glu Leu Ile Val Met Asn Ala Gly Pro Ala Leu  
 290 295 300

Tyr Ala Ala Asp Leu Ala Thr Ser Leu His Glu Gly Ile Gln Leu Ala  
 305 310 315 320

His Asp Ala Leu His Thr Gly Leu Ala Arg Glu Lys Met Asp Glu Leu  
 325 330 335

Val Ala Phe Thr Ala Val Tyr Arg Glu Glu Asn Ala Gln  
 340 345

<210> 3  
 <211> 918  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 3	
atggtcgaca aactgacgca cctgaaacag ctggaggcgg aaagcatcca catcatccgc	60
gaggtggccg ccgagttcga taacccggtg atgctgtact cgatcgcaa ggattccgcg	120
gtcatgctgc acctggcccg caaggccttc ttcccccggca agctgccctt cccggtgatg	180
cacgtggaca cccgctggaa attccaggag atgtacaggt tccgtgatcg gatggtcgag	240
gaaatgggcc tggatctgat caccacgac aacccggacg gcgtcgccca gggcatcaac	300
ccgttcaccc acggcagcgc caagcacacc gacgtgatga agaccgaggg actcaagcag	360
gccctggaca agtacggttt cgacgctgcc ttccggcggt cgccggcgcga cgaggagaag	420
tcgcgggcca aggaacgggt ctattcgttc cgcgacagca agcaccgctg ggacccgaag	480
aaccacgac cccgagctgtg gaacatctac aacggcaagg tgaagaaggg cgagtgcgtc	540
cgcgtcttcc cgctgtccaa ctggaccgag ctggacatct ggcaatacat ctacctggaa	600
ggcatcccga tcgtcccgct gtacttcgac gccgagcgcg aggtcatcgaa gaagaatggc	660
acattgatca tgatcgacga cgagcgcac ctcgagcatc tctctgacga agagaaagcc	720
cgcacatcgaga agcgcatggt ggcgttccgt accctcgct gctacccgct caccggcgcg	780
gtcgagtcga ggcgcaccac gctgccggaa atcatccagg aaatgctcct gacgcgtact	840
tccgaacgccc agggccgggt catcgaccat gaccaggccg gttcgatgga agaaaaagaaa	900
cgtcaggcgt atttctga	918

09743PC.ST25.txt

<210> 4  
<211> 305  
<212> PRT  
<213> *Pseudomonas aeruginosa*  
<400> 4

Met Val Asp Lys Leu Thr His Leu Lys Gln Leu Glu Ala Glu Ser Ile  
1 5 10 15

His Ile Ile Arg Glu Val Ala Ala Glu Phe Asp Asn Pro Val Met Leu  
20 25 30

Tyr Ser Ile Gly Lys Asp Ser Ala Val Met Leu His Leu Ala Arg Lys  
35 40 45

Ala Phe Phe Pro Gly Lys Leu Pro Phe Pro Val Met His Val Asp Thr  
50 55 60

Arg Trp Lys Phe Gln Glu Met Tyr Arg Phe Arg Asp Arg Met Val Glu  
65 70 75 80

Glu Met Gly Leu Asp Leu Ile Thr His Val Asn Pro Asp Gly Val Ala  
85 90 95

Gln Gly Ile Asn Pro Phe Thr His Gly Ser Ala Lys His Thr Asp Val  
100 105 110

Met Lys Thr Glu Gly Leu Lys Gln Ala Leu Asp Lys Tyr Gly Phe Asp  
115 120 125

Ala Ala Phe Gly Gly Ala Arg Arg Asp Glu Glu Lys Ser Arg Ala Lys  
130 135 140

Glu Arg Val Tyr Ser Phe Arg Asp Ser Lys His Arg Trp Asp Pro Lys  
145 150 155 160

Asn Gln Arg Pro Glu Leu Trp Asn Ile Tyr Asn Gly Lys Val Lys Lys  
165 170 175

Gly Glu Ser Ile Arg Val Phe Pro Leu Ser Asn Trp Thr Glu Leu Asp  
180 185 190

Ile Trp Gln Tyr Ile Tyr Leu Glu Gly Ile Pro Ile Val Pro Leu Tyr  
195 200 205

Phe Ala Ala Glu Arg Glu Val Ile Glu Lys Asn Gly Thr Leu Ile Met  
210 215 220

Ile Asp Asp Glu Arg Ile Leu Glu His Leu Ser Asp Glu Glu Lys Ala  
Page 4

225

230

09743PC.ST25.txt

235

240

Arg Ile Glu Lys Arg Met Val Arg Phe Arg Thr Leu Gly Cys Tyr Pro  
 245 250 255

Leu Thr Gly Ala Val Glu Ser Ser Ala Thr Thr Leu Pro Glu Ile Ile  
 260 265 270

Gln Glu Met Leu Leu Thr Arg Thr Ser Glu Arg Gln Gly Arg Val Ile  
 275 280 285

Asp His Asp Gln Ala Gly Ser Met Glu Glu Lys Lys Arg Gln Gly Tyr  
 290 295 300

Phe  
 305

<210> 5  
 <211> 822  
 <212> DNA  
 <213> *Pseudomonas aeruginosa*

<400> 5  
 atgaggccgg tgccttgggg cgaattggtg ggcgtggcgc ggcgcgcgg cgaggcgatc 60  
 ctgcccact ggcgcgcga cgtgggtggc cgctcgaagg ccgacgaatc gccggtgact 120  
 gccgcgcacc tggccgcgca ccatatattg gaggcgggat tgcggcgct ggcgcggac 180  
 attccgtgc tttccgaaga ggattgcgag ataccgctga gcgagcgcgg ccactggcgg 240  
 cgctggtggc tggggaccc gctggacggc accaaggagt tcatctccgg tagcgaggag 300  
 ttcaccgtca acgtggccct ggtcgaggat ggccgggtgc tggccgcct ggtcgccgt 360  
 ccggtgagcg gccgctgcta ctacggtggc gccggctcg gtgcctggcg cgaggaggcc 420  
 gatggccgcg cgcaaccgat cagtgtgcgc ctggagcccg aggaggcctt caccgtgg 480  
 gccagcaagc gccatggcag cccggcccgag gagcgcctgc tggatggctt gagcgagcgc 540  
 ttcggcgacc tgcggcgagc cagcatcgcc agttcgctga agttctgcct gctggccgag 600  
 ggcgctgccc actgctatcc ggcgcctgacg ccaacctcg aatggacac ggccgcgc 660  
 cagggtgtgc tggaaaggcgc cggccgcgag gtgcgcgacc tgcatggtgcc gccattcacc 720  
 tacgagccgc gcgaggatta cctcaacggc tccttcctgg ccctgcccgc cgccgcgc 780  
 tggcgcagcg agctgatcca actggcgccg cgcgtgcact ga 822

<210> 6  
 <211> 273  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*

<400> 6

## 09743PC.ST25.txt

Met Arg Pro Val Pro Trp Gly Glu Leu Val Ala Leu Val Arg Arg Ala  
1 5 10 15

Gly Glu Ala Ile Leu Pro His Trp Arg Ala Asp Val Val Val Arg Ser  
20 25 30

Lys Ala Asp Glu Ser Pro Val Thr Ala Ala Asp Leu Ala Ala His His  
35 40 45

Ile Leu Glu Ala Gly Leu Arg Ala Leu Ala Pro Asp Ile Pro Val Leu  
50 55 60

Ser Glu Glu Asp Cys Glu Ile Pro Leu Ser Glu Arg Gly His Trp Arg  
65 70 75 80

Arg Trp Trp Leu Val Asp Pro Leu Asp Gly Thr Lys Glu Phe Ile Ser  
85 90 95

Gly Ser Glu Glu Phe Thr Val Asn Val Ala Leu Val Glu Asp Gly Arg  
100 105 110

Val Leu Phe Gly Leu Val Gly Val Pro Val Ser Gly Arg Cys Tyr Tyr  
115 120 125

Gly Gly Ala Gly Leu Gly Ala Trp Arg Glu Glu Ala Asp Gly Arg Ala  
130 135 140

Gln Pro Ile Ser Val Arg Leu Glu Pro Glu Glu Ala Phe Thr Val Val  
145 150 155 160

Ala Ser Lys Arg His Gly Ser Pro Ala Gln Glu Arg Leu Leu Asp Gly  
165 170 175

Leu Ser Glu Arg Phe Gly Asp Leu Arg Arg Ala Ser Ile Gly Ser Ser  
180 185 190

Leu Lys Phe Cys Leu Leu Ala Glu Gly Ala Ala Asp Cys Tyr Pro Arg  
195 200 205

Leu Thr Pro Thr Ser Gln Trp Asp Thr Ala Ala Ala Gln Gly Val Leu  
210 215 220

Glu Gly Ala Gly Gly Glu Val Leu Asp Leu His Gly Ala Pro Phe Thr  
225 230 235 240

Tyr Glu Pro Arg Glu Asp Tyr Leu Asn Gly Ser Phe Leu Ala Leu Pro  
245 250 255

## 09743PC.ST25.txt

Arg Ala Ala Glu Trp Arg Ser Glu Leu Ile Gln Leu Ala Arg Ala Leu  
 260 265 270

His

<210> 7  
 <211> 1299  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 7  
 atgcgagttc tggtccttgg cagcgggtgtc atcgggtacccg ccagtgcgtttaacctggcc 60  
 cgtgccgggt tcgaggtgggt ggtgggtcgac cgtcaggacg gtcccgcgct ggaaaccaggc 120  
 ttgcggcaacg ccggccagggt gtctcccggc tacgcttcgc cctgggcagc cccgggcatt 180  
 cccctgaagg ccatgaagtg gctgctggaa aagcacgcgc cgtggccat caagctcacc 240  
 tccgatccca gccagttacgc ctggatgctg cagatgctgc gcaactgcac cgccgagcgc 300  
 tacgcccgtga acaaggagcg catggtccgc ctgtccgagt acagccgcga ttgcctcgac 360  
 gaactgcgcg ccgagaccgg catcgctac gagggccgca ccctcgac caccctactg 420  
 ttccgcaccc aggcgcagct ggacgcccggc ggcaaggaca tcgccgtgct cgagcgctcc 480  
 ggcgtgcgc acgagggttct cgaccgcgac ggcatcgccc gcgttagagcc ggctttggcc 540  
 aagggtcgccg acaagctggt cggcgcttg cgcctgcacca acgaccagac cggcgactgc 600  
 cagctgttca ccacccgcct ggcggaaatg gccaagggcc tggcgtgga gttccgccttc 660  
 ggccagaaca tcgagcgccct ggacttcgccc ggcgaccgca tcaacggcgt gctggtcaac 720  
 ggcgaattgc tcaccgcgc ccactacgtg ctggccctgg gcagctactc gccgcaactg 780  
 ctcaaggccgc tgggtatcaa ggctccggtc tatccgctga agggttattc gctgaccgtg 840  
 ccgatcacca accccggagat ggcggccgacc tcgaccatcc tcgacgagac ctacaaggtg 900  
 gcgatcaccc gcttcgacca ggcgcattccgc gtcggcggca tggcggaaat cgccggcttc 960  
 gacctgtcgc tgaacccgcg ccgcgcgag accctggaaa tgatcaccac cgacctctat 1020  
 cccgagggcg gcgatatacg ccaggcgacc ttctggaccg gcctgcgcggc ggcgaccccg 1080  
 gatggcaccc cgatcgtcgg cgccacccgc taccgcaacc tggcgttccaa taccggccac 1140  
 ggcaccctgg gttggaccat ggcctgcggg tcgggtcgct acctggccga cctgatggcg 1200  
 aagaagcgcc cgcagatcag taccgaaggc ctggatattt cccgctacag caattccccg 1260  
 gagaacgcca agaatgccccca tccagcgcca gcacactaa 1299

<210> 8  
 <211> 432  
 <212> PRT  
 <213> Pseudomonas aeruginosa

## 09743PC.ST25.txt

&lt;400&gt; 8

Met Arg Val Leu Val Leu Gly Ser Gly Val Ile Gly Thr Ala Ser Ala  
1 5 10 15

Tyr Tyr Leu Ala Arg Ala Gly Phe Glu Val Val Val Val Asp Arg Gln  
20 25 30

Asp Gly Pro Ala Leu Glu Thr Ser Phe Ala Asn Ala Gly Gln Val Ser  
35 40 45

Pro Gly Tyr Ala Ser Pro Trp Ala Ala Pro Gly Ile Pro Leu Lys Ala  
50 55 60

Met Lys Trp Leu Leu Glu Lys His Ala Pro Leu Ala Ile Lys Leu Thr  
65 70 75 80

Ser Asp Pro Ser Gln Tyr Ala Trp Met Leu Gln Met Leu Arg Asn Cys  
85 90 95

Thr Ala Glu Arg Tyr Ala Val Asn Lys Glu Arg Met Val Arg Leu Ser  
100 105 110

Glu Tyr Ser Arg Asp Cys Leu Asp Glu Leu Arg Ala Glu Thr Gly Ile  
115 120 125

Ala Tyr Glu Gly Arg Thr Leu Gly Thr Thr Gln Leu Phe Arg Thr Gln  
130 135 140

Ala Gln Leu Asp Ala Ala Gly Lys Asp Ile Ala Val Leu Glu Arg Ser  
145 150 155 160

Gly Val Pro Tyr Glu Val Leu Asp Arg Asp Gly Ile Ala Arg Val Glu  
165 170 175

Pro Ala Leu Ala Lys Val Ala Asp Lys Leu Val Gly Ala Leu Arg Leu  
180 185 190

Pro Asn Asp Gln Thr Gly Asp Cys Gln Leu Phe Thr Thr Arg Leu Ala  
195 200 205

Glu Met Ala Lys Gly Leu Gly Val Glu Phe Arg Phe Gly Gln Asn Ile  
210 215 220

Glu Arg Leu Asp Phe Ala Gly Asp Arg Ile Asn Gly Val Leu Val Asn  
225 230 235 240

Gly Glu Leu Leu Thr Ala Asp His Tyr Val Leu Ala Leu Gly Ser Tyr  
Page 8

245

09743PC.ST25.txt

250

255

Ser Pro Gln Leu Leu Lys Pro Leu Gly Ile Lys Ala Pro Val Tyr Pro  
 260 265 270

Leu Lys Gly Tyr Ser Leu Thr Val Pro Ile Thr Asn Pro Glu Met Ala  
 275 280 285

Pro Thr Ser Thr Ile Leu Asp Glu Thr Tyr Lys Val Ala Ile Thr Arg  
 290 295 300

Phe Asp Gln Arg Ile Arg Val Gly Gly Met Ala Glu Ile Ala Gly Phe  
 305 310 315 320

Asp Leu Ser Leu Asn Pro Arg Arg Arg Glu Thr Leu Glu Met Ile Thr  
 325 330 335

Thr Asp Leu Tyr Pro Glu Gly Gly Asp Ile Ser Gln Ala Thr Phe Trp  
 340 345 350

Thr Gly Leu Arg Pro Ala Thr Pro Asp Gly Thr Pro Ile Val Gly Ala  
 355 360 365

Thr Arg Tyr Arg Asn Leu Phe Leu Asn Thr Gly His Gly Thr Leu Gly  
 370 375 380

Trp Thr Met Ala Cys Gly Ser Gly Arg Tyr Leu Ala Asp Leu Met Ala  
 385 390 395 400

Lys Lys Arg Pro Gln Ile Ser Thr Glu Gly Leu Asp Ile Ser Arg Tyr  
 405 410 415

Ser Asn Ser Pro Glu Asn Ala Lys Asn Ala His Pro Ala Pro Ala His  
 420 425 430

<210> 9  
 <211> 771  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 9  
 atggcactgg caaaacgcacat catccccgtgc ctcgacgtgg acaacggcccg agtgggtcaag 60  
 ggcgtcaagt tcgagaacat ccgcgcacgccc ggcgaccggcgg tcgagatcgc tcggccgtac 120  
 gacgagcagg gtgccgacga gatcaccttc ctcgatatac cccgcccacgt cgacgggcgc 180  
 gacaccaccc tgcataccgt cgagcgcacg gctagccagg tggccattcc gctgaccgtg 240  
 ggcggccggcg tacgcagcgt gcaggacatc cgcaacctgt tgaatgccgg cgccggacaag 300  
 gtctcgatca acaccgcccgc ggtgttcaac cccgagttcg tcggtgaggc cgccgaccgc 360

## 09743PC.ST25.txt

ttcggctcgc agtgcacatcg	ggtcgcccatt	gacgcgaaga aggtttccgc	cccgggcgag	420
gcccgcgtt gggaaatctt	cacccatggc	ggcgcaagc ccaccgggct	ggatgccgtg	480
ctctggcgaa agaagatgga	agacttggc	gctggcgaga ttctcctgac	cagcatggac	540
caggacggcg tgaagagcgg	ttacgacctg	ggcgtgaccc gcgcattcag	cgaggcggtg	600
aacgtgcccgg tgatcgcttc	cggcggcgtc	ggcaacctgg agcacctggc	cgccggcattc	660
ctcgaggcga aggccgacgc	ggtgctcgcg	gcgagcatct tccacttcgg	cgagtacacc	720
gtgcccgaag ccaaggccta	cctggccagc	cgcggtatcg tggtgcgctg	a	771

<210> 10  
 <211> 256  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*

<400> 10

Met Ala Leu Ala Lys Arg Ile Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15

Arg Val Val Lys Gly Val Lys Phe Glu Asn Ile Arg Asp Ala Gly Asp  
 20 25 30

Pro Val Glu Ile Ala Arg Arg Tyr Asp Glu Gln Gly Ala Asp Glu Ile  
 35 40 45

Thr Phe Leu Asp Ile Thr Ala Ser Val Asp Gly Arg Asp Thr Thr Leu  
 50 55 60

His Thr Val Glu Arg Met Ala Ser Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80

Gly Gly Gly Val Arg Ser Val Gln Asp Ile Arg Asn Leu Leu Asn Ala  
 85 90 95

Gly Ala Asp Lys Val Ser Ile Asn Thr Ala Ala Val Phe Asn Pro Glu  
 100 105 110

Phe Val Gly Glu Ala Ala Asp Arg Phe Gly Ser Gln Cys Ile Val Val  
 115 120 125

Ala Ile Asp Ala Lys Lys Val Ser Ala Pro Gly Glu Ala Pro Arg Trp  
 130 135 140

Glu Ile Phe Thr His Gly Gly Arg Lys Pro Thr Gly Leu Asp Ala Val  
 145 150 155 160

Leu Trp Ala Lys Lys Met Glu Asp Leu Gly Ala Gly Glu Ile Leu Leu  
 Page 10

165

09743PC.ST25.txt

170

175

Thr Ser Met Asp Gln Asp Gly Val Lys Ser Gly Tyr Asp Leu Gly Val  
 180 185 190

Thr Arg Ala Ile Ser Glu Ala Val Asn Val Pro Val Ile Ala Ser Gly  
 195 200 205

Gly Val Gly Asn Leu Glu His Leu Ala Ala Gly Ile Leu Glu Gly Lys  
 210 215 220

Ala Asp Ala Val Leu Ala Ala Ser Ile Phe His Phe Gly Glu Tyr Thr  
 225 230 235 240

Val Pro Glu Ala Lys Ala Tyr Leu Ala Ser Arg Gly Ile Val Val Arg  
 245 250 255

<210> 11  
 <211> 1035  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 11  
 atgatcaagg tcggcatcg tggcggtacg ggttatacgg gcgtggaact gctgcgcctg 60  
 ctggcgccagc atccgcaggc ccgggtggaa gtgatcactt cgcgttccga ggcgggggtg 120  
 aaggtcgccc acatgtaccc gaacctgcga ggtcattatg acgacctgca gttcagcgtg 180  
 ccggacgcgc agcgcctcgg cgcctgcgac gtgggttct tcgcccacgccc gcacggcgtg 240  
 ggcgcacgcgc tggctggcga actgctggac gcccggaccc gggtcatcga tctgtccgct 300  
 gacttccgccc tggcggacgc cgaggagtgg gcgcgctggt acggccagcc gcatggcgct 360  
 ccggcgctgc tcgacgaggc tgtctacggc ctgcccggaa tgaaccgcga gaagatccgc 420  
 caggcccccc tgatcgccgt gcccggctgc taccggaccg cgacccagct gggcctgatc 480  
 ccgctgctgg aagccggcct gcccgcgc tcgcccggta tcgcccattt caagtccggg 540  
 gtcagcgggtg ccggcggggg cgccaaagggtt ggctcgctgt tctgcgaggc gggcgaaagc 600  
 atgatggcct acgcggtaa agggcatcg catctccgg aaatcagccca gggcctgcgt 660  
 cgggcctccg gcccgcacgt cgggctgcacg ttgcgtaccgc acctgacgc aatgatccgc 720  
 ggtatccatg caaccctcta tgcccatgtc gcggatcgct cggatcgaccc ccaggcggtt 780  
 ttgcagaaggc gctacgcgcga cgaacccttc gtcgacgtga tgccggccgg cagccatccg 840  
 gagacccgcga gcgtgcgtgg cgccaaatgtc tgccgaatcg ccgtgcaccc cccccagggc 900  
 ggcgcacccgg tggtggtgt gtcgggtatc gacaacctgg tcaagggcgc ctcgggtcag 960  
 gcgctccaga acatgaacat cctgttcggg ctggacgagc gcctggccct ctcgcattgcg 1020  
 gcccctgcgtcc cctga 1035

09743PC.ST25.txt

<210> 12  
<211> 344  
<212> PRT  
<213> *Pseudomonas aeruginosa*

<400> 12

Met Ile Lys Val Gly Ile Val Gly Gly Thr Gly Tyr Thr Gly Val Glu  
1 5 10 15

Leu Leu Arg Leu Leu Ala Gln His Pro Gln Ala Arg Val Glu Val Ile  
20 25 30

Thr Ser Arg Ser Glu Ala Gly Val Lys Val Ala Asp Met Tyr Pro Asn  
35 40 45

Leu Arg Gly His Tyr Asp Asp Leu Gln Phe Ser Val Pro Asp Ala Gln  
50 55 60

Arg Leu Gly Ala Cys Asp Val Val Phe Phe Ala Thr Pro His Gly Val  
65 70 75 80

Ala His Ala Leu Ala Gly Glu Leu Leu Asp Ala Gly Thr Arg Val Ile  
85 90 95

Asp Leu Ser Ala Asp Phe Arg Leu Ala Asp Ala Glu Glu Trp Ala Arg  
100 105 110

Trp Tyr Gly Gln Pro His Gly Ala Pro Ala Leu Leu Asp Glu Ala Val  
115 120 125

Tyr Gly Leu Pro Glu Val Asn Arg Glu Lys Ile Arg Gln Ala Arg Leu  
130 135 140

Ile Ala Val Pro Gly Cys Tyr Pro Thr Ala Thr Gln Leu Gly Leu Ile  
145 150 155 160

Pro Leu Leu Glu Ala Gly Leu Ala Asp Ala Ser Arg Leu Ile Ala Asp  
165 170 175

Cys Lys Ser Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Val Gly Ser  
180 185 190

Leu Phe Cys Glu Ala Gly Glu Ser Met Met Ala Tyr Ala Val Lys Gly  
195 200 205

His Arg His Leu Pro Glu Ile Ser Gln Gly Leu Arg Arg Ala Ser Gly  
210 215 220

## 09743PC.ST25.txt

Gly Asp Val Gly Leu Thr Phe Val Pro His Leu Thr Pro Met Ile Arg  
 225 230 235 240

Gly Ile His Ala Thr Leu Tyr Ala His Val Ala Asp Arg Ser Val Asp  
 245 250 255

Leu Gln Ala Leu Phe Glu Lys Arg Tyr Ala Asp Glu Pro Phe Val Asp  
 260 265 270

Val Met Pro Ala Gly Ser His Pro Glu Thr Arg Ser Val Arg Gly Ala  
 275 280 285

Asn Val Cys Arg Ile Ala Val His Arg Pro Gln Gly Gly Asp Leu Val  
 290 295 300

Val Val Leu Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln  
 305 310 315 320

Ala Leu Gln Asn Met Asn Ile Leu Phe Gly Leu Asp Glu Arg Leu Gly  
 325 330 335

Leu Ser His Ala Ala Leu Leu Pro  
 340

<210> 13  
 <211> 1644  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 13	
gtgagcgaac tcattcgcgt acccgacatc ggcaacggtg agggtaagt catcgagctg	60
ctggtaaggc cggcgacaa ggtcgaggcc gatcagagcc tgctgaccct ggaatccgac	120
aaggccagca tggaaatccc cagtcggaaag gcccgggtag tgaaaagcat caaggcgaag	180
gtcggcgaca cttgaaaga aggtgacgaa atcctcgagc tggaagtggaa aggcggcgaa	240
cagcctgccc aagccaaggc cgaggcagcg cccgccccaaac cggaagcgcc gaaagccgaa	300
gcgcctgctc cggccccgag cgagagcaag cggccggccc cggccgcggc cagcgtccag	360
gacatcaagg tcccgacat cggctcgcc ggcaaggcca acgtcatcga agtgatggtc	420
aaggccggcg acacggtcga ggcggaccag tcgctgatca ccctgaaatc cgacaaggcc	480
agcatggaga tcccctcgcc ggcctccggg gtggtgaaaa gcgtctcgat caaggtcggt	540
gacgaagtcg gcaccggcga cctgatcctc aagctgaagg tggaaggcgc cgctccggca	600
gccgaagagc aaccggcagc cgctccggcc caggccgcgg cgccccccgc cgagcagaag	660
cccgccgcgg cggccccctgc gccagccaag gccgataaccc cggctccgggt cggcgcaccc	720
agccgcgacg gcgccaaggt ccacgcccggc cggcgggtgc gcatgctggc gcgcgagttc	780

## 09743PC.ST25.txt

ggcgtcgagc	tgagcgaagt	gaaagccagc	ggtcccaagg	gtcgcatcct	caaggaagac	840
gtccaggcct	tcgtcaagga	gcaactgcag	cgcgccaagt	ccggcggtgc	cggcgccacc	900
ggcggagccg	gcatcccgcc	gatccggaa	gtcgacttca	gcaagttcgg	cgaagtggaa	960
gaagtggcga	tgacccgcct	gatgcaggtc	ggcgcccca	acctgcatcg	cagctggctg	1020
aacgtgccgc	acgtgaccca	gttcgaccag	tcggacatca	ccgacatgga	agcctccgc	1080
gttgcccaga	aggccgcggc	ggagaaggcc	ggggtcaagc	tgaccgtact	gccgatcctg	1140
ctcaaggcct	gcccacact	gctcaaggaa	ctgccggact	tcaacagttc	gctggccccc	1200
agcggcaagg	cgctgatccg	caagaagtac	gtacacatcg	gcttcgcccgt	ggacactccg	1260
gacggcctgc	tggtcccggt	gatccgcgt	gtcgaccgga	agagcctcct	gcaactggcc	1320
gccgaggccg	ccgacctggc	cgacaaggcc	cgcaacaaga	agctctcggc	cgatgccatg	1380
cagggcgccct	gcttcaccat	ctccagtctc	ggccacatcg	gcccacccgg	cttcacgccc	1440
atcgtcaacg	cgccggaagt	ggcgatcctc	ggtgtgtcca	aggcgaccat	gcagccggt	1500
tgggacggca	aggcattcca	gccgcgcctg	atgctccgc	tgtcgctgtc	ctacgaccat	1560
cgcgtgatca	acggtgccgc	cgcggcgccgc	ttcaccaagc	gcctggcga	gctgctggcg	1620
gacatccgca	ccctgctcct	gtaa				1644

<210> 14  
 <211> 547  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*

<400> 14

Met Ser Glu Leu Ile Arg Val Pro Asp Ile Gly Asn Gly Glu Gly Glu  
 1 5 10 15

Val Ile Glu Leu Leu Val Lys Pro Gly Asp Lys Val Glu Ala Asp Gln  
 20 25 30

Ser Leu Leu Thr Leu Glu Ser Asp Lys Ala Ser Met Glu Ile Pro Ser  
 35 40 45

Pro Lys Ala Gly Val Val Lys Ser Ile Lys Ala Lys Val Gly Asp Thr  
 50 55 60

Leu Lys Glu Gly Asp Glu Ile Leu Glu Leu Glu Val Glu Gly Gly Glu  
 65 70 75 80

Gln Pro Ala Glu Ala Lys Ala Glu Ala Ala Pro Ala Gln Pro Glu Ala  
 85 90 95

Pro Lys Ala Glu Ala Pro Ala Pro Ser Glu Ser Lys Pro Ala  
 Page 14

100

09743PC.ST25.txt

105

110

Ala Pro Ala Ala Ala Ser Val Gln Asp Ile Lys Val Pro Asp Ile Gly  
115 120 125

Ser Ala Gly Lys Ala Asn Val Ile Glu Val Met Val Lys Ala Gly Asp  
130 135 140

Thr Val Glu Ala Asp Gln Ser Leu Ile Thr Leu Glu Ser Asp Lys Ala  
145 150 155 160

Ser Met Glu Ile Pro Ser Pro Ala Ser Gly Val Val Glu Ser Val Ser  
165 170 175

Ile Lys Val Gly Asp Glu Val Gly Thr Gly Asp Leu Ile Leu Lys Leu  
180 185 190

Lys Val Glu Gly Ala Ala Pro Ala Ala Glu Glu Gln Pro Ala Ala Ala  
195 200 205

Pro Ala Gln Ala Ala Ala Pro Ala Ala Glu Gln Lys Pro Ala Ala Ala  
210 215 220

Ala Pro Ala Pro Ala Lys Ala Asp Thr Pro Ala Pro Val Gly Ala Pro  
225 230 235 240

Ser Arg Asp Gly Ala Lys Val His Ala Gly Pro Ala Val Arg Met Leu  
245 250 255

Ala Arg Glu Phe Gly Val Glu Leu Ser Glu Val Lys Ala Ser Gly Pro  
260 265 270

Lys Gly Arg Ile Leu Lys Glu Asp Val Gln Val Phe Val Lys Glu Gln  
275 280 285

Leu Gln Arg Ala Lys Ser Gly Gly Ala Gly Ala Thr Gly Gly Ala Gly  
290 295 300

Ile Pro Pro Ile Pro Glu Val Asp Phe Ser Lys Phe Gly Glu Val Glu  
305 310 315 320

Glu Val Ala Met Thr Arg Leu Met Gln Val Gly Ala Ala Asn Leu His  
325 330 335

Arg Ser Trp Leu Asn Val Pro His Val Thr Gln Phe Asp Gln Ser Asp  
340 345 350

Ile Thr Asp Met Glu Ala Phe Arg Val Ala Gln Lys Ala Ala Ala Glu  
Page 15

355

360

365

09743PC.ST25.txt

Lys Ala Gly Val Lys Leu Thr Val Leu Pro Ile Leu Leu Lys Ala Cys  
 370 375 380

Ala His Leu Leu Lys Glu Leu Pro Asp Phe Asn Ser Ser Leu Ala Pro  
 385 390 395 400

Ser Gly Lys Ala Leu Ile Arg Lys Lys Tyr Val His Ile Gly Phe Ala  
 405 410 415

Val Asp Thr Pro Asp Gly Leu Leu Val Pro Val Ile Arg Asp Val Asp  
 420 425 430

Arg Lys Ser Leu Leu Gln Leu Ala Ala Glu Ala Ala Asp Leu Ala Asp  
 435 440 445

Lys Ala Arg Asn Lys Lys Leu Ser Ala Asp Ala Met Gln Gly Ala Cys  
 450 455 460

Phe Thr Ile Ser Ser Leu Gly His Ile Gly Gly Thr Gly Phe Thr Pro  
 465 470 475 480

Ile Val Asn Ala Pro Glu Val Ala Ile Leu Gly Val Ser Lys Ala Thr  
 485 490 495

Met Gln Pro Val Trp Asp Gly Lys Ala Phe Gln Pro Arg Leu Met Leu  
 500 505 510

Pro Leu Ser Leu Ser Tyr Asp His Arg Val Ile Asn Gly Ala Ala Ala  
 515 520 525

Ala Arg Phe Thr Lys Arg Leu Gly Glu Leu Leu Ala Asp Ile Arg Thr  
 530 535 540

Leu Leu Leu  
 545

<210> 15  
 <211> 996  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 15  
 atgagttggc tgactccccgc tctggtcacc atcatcctca ccgtggtcaa ggccatcg 60  
 gtgctgctcg ccgtggtcat ctgcggcgcc ctgctaagct gggtcgagcg ccgcctgctc 120  
 ggcctctggc aggaccgcta cggcccaac cgggtcggtc cgttcggtgc gttccagctc 180  
 ggcgcggaca tggtaagat gttcttcaag gaggactgga ccccgccgtt cgccgacaag 240

## 09743PC.ST25.txt

atgatcttca	ccctggcccc	ggtaatcgcg	atgggcgc	tgctcg	tcgc	cttcgc	ccatc	300
gtgccgatca	cccccacctg	gggcgtggcg	gacctgaaca	tcggcatc	cct	ttcttcttc		360
gccatggccg	gcctgacggt	gtacgcccgt	ctgttcgc	gctgg	tcgag	caacaacaag		420
ttcgccctgc	tcggcagc	cgt	gcgcgc	cgt	gccc	agac	atcg	480
gccc	gtcg	tgatgg	catcg	tcgg	ctcg	tcaacat	cgacatcg	540
cagtaccaga	tcgaca	acgt	ctgg	ttcatc	attcc	cgagt	tcttcgg	600
atcatcgccg	gcgtcg	ccgt	gacc	accgt	cacc	cgtt	cttcgg	660
gaactggcgg	acgg	ctacca	catcg	agtc	ccggat	aatgggg	catcg	720
ggc	gagt	taca	tcgg	catcg	actgg	tcgt	gctgtt	780
tggcacgg	tc	cg	ttc	cgtt	gccc	ctt	tcgtt	840
accgg	ttct	tc	atc	atcg	atcc	cg	ccgtat	900
gaccagg	gt	tg	gc	ttc	gat	tg	accctg	960
gtgaccgg	cg	ct	cg	tg	gt	ca	acc	
								996

<210> 16  
 <211> 331  
 <212> PRT  
 <213> Pseudomonas aeruginosa  
  
 <400> 16

Met Ser Trp Leu Thr Pro Ala Leu Val Thr Ile Ile Leu Thr Val Val  
 1 5 10 15

Lys Ala Ile Val Val Leu Leu Ala Val Val Ile Cys Gly Ala Leu Leu  
 20 25 30

Ser Trp Val Glu Arg Arg Leu Leu Gly Leu Trp Gln Asp Arg Tyr Gly  
 35 40 45

Pro Asn Arg Val Gly Pro Phe Gly Ala Phe Gln Leu Gly Ala Asp Met  
 50 55 60

Val Lys Met Phe Phe Lys Glu Asp Trp Thr Pro Pro Phe Ala Asp Lys  
 65 70 75 80

Met Ile Phe Thr Leu Ala Pro Val Ile Ala Met Gly Ala Leu Leu Val  
 85 90 95

Ala Phe Ala Ile Val Pro Ile Thr Pro Thr Trp Gly Val Ala Asp Leu  
 100 105 110

Asn Ile Gly Ile Leu Phe Phe Ala Met Ala Gly Leu Thr Val Tyr  
 Page 17

115

120

09743PC.ST25.txt

125

Ala Val Leu Phe Ala Gly Trp Ser Ser Asn Asn Lys Phe Ala Leu Leu  
 130 135 140

Gly Ser Leu Arg Ala Ser Ala Gln Thr Ile Ser Tyr Glu Val Phe Leu  
 145 150 155 160

Ala Leu Ser Leu Met Gly Ile Val Ala Gln Val Gly Ser Phe Asn Met  
 165 170 175

Arg Asp Ile Val Gln Tyr Gln Ile Asp Asn Val Trp Phe Ile Ile Pro  
 180 185 190

Gln Phe Phe Gly Phe Cys Thr Phe Ile Ile Ala Gly Val Ala Val Thr  
 195 200 205

His Arg His Pro Phe Asp Gln Pro Glu Ala Glu Gln Glu Leu Ala Asp  
 210 215 220

Gly Tyr His Ile Glu Tyr Ala Gly Met Lys Trp Gly Met Phe Phe Val  
 225 230 235 240

Gly Glu Tyr Ile Gly Ile Val Leu Val Ser Ala Leu Leu Ala Thr Leu  
 245 250 255

Phe Phe Gly Gly Trp His Gly Pro Phe Leu Asp Thr Leu Pro Trp Leu  
 260 265 270

Ser Phe Phe Tyr Phe Ala Ala Lys Thr Gly Phe Phe Ile Met Leu Phe  
 275 280 285

Ile Leu Ile Arg Ala Ser Leu Pro Arg Pro Arg Tyr Asp Gln Val Met  
 290 295 300

Ala Phe Ser Trp Lys Val Cys Leu Pro Leu Thr Leu Ile Asn Leu Leu  
 305 310 315 320

Val Thr Gly Ala Leu Val Leu Ala Ala Gln  
 325 330

<210> 17  
 <211> 7347  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 17  
 gtgcgaagcac tcatagagaaa ggtgggctcc ctttcccccc aggaaaggaa ggcattggct 60  
 gtcctgctca agcagcaagg tgtcaatctc ttcgagatcg cgccagtgtt caagcgccag 120

## 09743PC.ST25.txt

gacggcgagc	ccctcgccgt	ctcctatgcc	caggagcgac	agtggttct	ctggcaactg	180
gagccggaaa	gcgcggccct	ccatatcccc	agtgtcttgc	gtctacgtgg	gcggctggac	240
ctggatgccc	tgcaacgcag	cttcgacagc	ctgggtgcgc	ggcacgagac	cctacgcacc	300
cgtttcgccc	tcgacggcga	cgaggcgccg	caggagatcg	ccgcattccat	ggcattgccc	360
ttggatatacg	tcgcgttggg	gccgctcgag	gagggcgc	tcgctcggca	ggtcgagacg	420
acgatcgccg	ggccgttcga	cctggagcgt	ggccgcgtgc	tgcggtgag	cctgttgcgg	480
ctggccgagg	acgaccatgt	gctggtgctg	gtccagcatc	acatcggtc	cgacggttgg	540
tcgatgcagg	tgatggtcga	ggaactggtc	cagctctatg	ccgcctata	tcgagggctc	600
gaggtagcgc	tgccggctt	gccgatccag	tacgcggact	acgcctgtg	gcagcgcagc	660
tggatggagg	ccggggaaaa	ggagcgcag	ttggcgta	ggaccggcct	gctggcggc	720
gagcagccgg	tgctggagtt	gccgttcgac	cggccgcgc	cggttgcggca	aagccatcgt	780
ggtgcccagt	tcatcctgga	actggatatt	gatctgtccc	aggcgtcag	gcgcgtggcc	840
cagcaggagg	gggctactgc	cttcgcctg	ttgctggctt	cgttccaggc	gctgctgtat	900
cgctacagcg	ggcaggcgga	tatccgtgtc	ggcgtgccga	tcgccaatcg	caaccgcgtg	960
gagaccgagc	ggctgatcgg	cttcttcgtc	aacacccagg	tgctcaaggc	cgacctggac	1020
ggtcggatgg	gcttcgacga	gctgctggcc	caggcccgc	aacgcgcgt	ggaggcccag	1080
gcgcaccagg	acctgcccgtt	cgagcaactg	gtggaggcct	tgcagccgga	gcgcagtctt	1140
agccacaacc	cgctgttcca	ggtgctgttc	aactaccaga	gcgaagcccg	tggcaacggc	1200
caggcattcc	gttgcacga	gttacagatg	gaaagcgtgc	attcgcacag	ccggacggcg	1260
cagttcgact	tgacgttgg	cctgacggac	gaagagcagc	gttttgcgc	cgtttgcac	1320
tacgccaccg	acctgttca	cgcctccacc	gtggAACGCC	tggccggcca	ttggcgcaac	1380
ctgttgcgcg	gcatcgtcgc	caacccacga	cagcggctcg	gcgagttgcc	gctgctggat	1440
gcgcgggagc	gccggcagac	cctctccgaa	tggAACCCGG	cccagcgcga	gtgcgcggtg	1500
cagggcacct	tgcagcagcg	tttcgaggaa	caggcgccgc	aacggccaca	ggcggttgcg	1560
ctgatcctcg	acgaacaacg	gttgagctac	ggcgaactga	atgcgcgggc	caatcgctg	1620
gcgcactgcc	tgatcgcccg	tggcggttgc	gcggacgtgc	cggtcgggct	ggcgctggag	1680
cgttcgctgg	acatgctgg	cggcttgcgt	gcatcctca	aggcggcgg	cgcctacctg	1740
ccgttggacc	cggcgccgccc	agaggagcgc	ctggcgacata	tcctcgacga	cagtgggt	1800
cggctgctgc	tgacccaggg	gcatctgctc	gagcgcctgc	cacggcaggc	gggggtggag	1860
gtgctggcca	tgcacggact	ggtgctggac	ggctacgccc	agagcgatcc	gtccccacg	1920
ctatcgccgg	acaacctggc	ctacgtgatc	tatacctcgg	gctcgaccgg	caagcccaag	1980
ggcacattgc	tcacccaccc	caacgcgcgt	cgcctgttca	gcgcaccgg	ggcctgggtc	2040

## 09743PC.ST25.txt

ggcttcgacg	agcgggacgt	gtggacattg	ttccattcct	acgccttcga	tttctcggtc	2100
tgggaaatct	tcggcgcgct	gctctatggc	gggtgcctgg	tgattgtgcc	gcaatgggtg	2160
agccgttcgc	cggaagactt	ctaccgtctg	ctgtgcccg	aaggcgtgac	ggtgctcaac	2220
cagacgcccgt	cggcgttcaa	gcaactgatg	gcgggtggcct	gttccgcccga	catggcgacg	2280
cagcagccgg	cgctgcgcta	cgtgatcttc	ggtggcgagg	cgctggatct	gcagagcctg	2340
cggccgtggt	tccagcgctt	cggcgatcgc	cagccgcaac	tggtaacat	gtacggcattc	2400
accgagacca	cggtgcacgt	aacctaccgt	ccggtgagcg	aggccgacct	ggaagggtggc	2460
ctggtcagtc	cgattggcg	gaccatcccg	gacctgtcct	ggtacatcct	cgaccgtgac	2520
ctgaacccgg	tgccgcgcgg	cgggtgggc	gagctgtaca	tcggtcgcgc	cgggctggcg	2580
cgcggctacc	tgaggcggcc	cgggttgagt	gccacccgct	tcgtgcccggaa	cccggtcccc	2640
ggcggcgccg	gcgagcggct	gtaccgtacc	ggcgacctgg	cacggttcca	ggcggatggc	2700
aatatcgagt	acatcggcg	tatcgaccac	caggtgaagg	ttcgcggctt	ccgtatcgaa	2760
ctgggcgaga	tcgaagcggc	gctgcgggt	ctggccgggg	tacgcgatgc	cgtggtgctg	2820
gcccattgacg	gagtcggcg	cacgcaactg	gtgggatacg	tgggtggcgga	ctcggcgag	2880
gatgccgagc	gtctgcggga	gtcgctgcgg	gagtcgctga	agcggcacct	gccggactac	2940
atgggtccgg	cgcacactgat	gctgctggag	cgatgcccgc	tgacggtcaa	tggcaagctc	3000
gaccggcagg	cgttgcgcga	accggatgcg	agcctgtcgc	aacaggccta	tcgagcggccc	3060
ggtagcggc	tggagcagcg	catcgacgc	atctggtcgg	agatcctggg	agtggAACGG	3120
gtcggcctgg	acgacaactt	cttcgaactg	ggcggtcatt	cgttgctggc	tacccgggtg	3180
atttctcggg	ttcgcgcagga	gcagcagttg	gacgcaagcc	tgaaggcggt	gttcgagcgg	3240
ccgggtctgg	aagcggtcgc	ccagggattt	gaacgcacga	cggatgcgg	ctcgacgata	3300
ccgcttgccg	atcggcagca	accgttggca	ctgtccttcg	ctcaggagcg	tcagtggttc	3360
ctctggcaac	tggagccgg	aagcgcggcc	taccatattc	cgagtgcctt	gcgcctacgc	3420
ggcgccgtgg	acgtggatgc	cttgcacgc	agcttcgaca	gcctggtcgc	gcggcatgaa	3480
accttgcgta	cccgcttcg	gctggaggga	ggcggttcgt	accagcaggt	acaacctgcg	3540
gttagcgttt	ccatcgacgc	ggaacacgttc	ggtgaagaag	gcctgatcga	acggatacag	3600
gccatcgttt	tgcagccatt	cgacactggaa	cggggccgc	tgctgcgggt	gaacctgttg	3660
caacttggccg	aggacgacca	tgtactggtg	ctggtccagc	accacatcgt	gtccgatgg	3720
tggtcgatgc	aggtgatggt	cgagggactg	gtccagctct	atgccccta	tagccaagg	3780
ctcgacgtgg	tgttgccagc	cctgcccgc	cagtacgcgg	actacgcctt	gtggcagcgc	3840
agctggatgg	aggcggggg	aaaggagcgc	cagttggcgt	actggaccgg	cctgctgggc	3900
ggcgagcagc	cggtgctgga	gttgcgcgtt	gatcggccgc	gtccggcccg	gcagagccat	3960

## 09743PC.ST25.txt

cgtggcgcbc	agttgggttt	cgagctatcg	cgggaactgg	tcgaggccgt	gagagccttg	4020
gcccagcgtg	aaggcgccag	tagtttcatg	ctgttgcgtgg	cctcggttcca	ggcgctgttg	4080
tatcgctaca	gcgggcaggc	ggatatccgt	gtcgggtgtgc	cgatcgccaa	tcgcaaccgc	4140
gtggagaccc	agcggctgtat	cggcttcttc	gtcaacacccc	aggtgctcaa	ggccgacactg	4200
gacggtcgga	tgggcttcga	cgagctgctg	gcccaggccc	gccaacgcgc	gctggaggcc	4260
caggcgcacc	aggacctgcc	gttcgagcaa	ctgggtggaaag	ccttgcagcc	ggagcgcaat	4320
gccagccaca	acccactgtt	ccaggtgctg	ttcaaccatc	agagcgagat	acgctcggtg	4380
acgcccggagg	ttcagttgga	ggacctgcgt	ctggaaaggcc	tggcctggga	cggccagact	4440
gcgcagttcg	acctgacgct	ggatattcag	gaagacgaaa	acggcatctg	ggcctcccttc	4500
gactatgcca	ccgatctgtt	cgacgcctcc	accgtggaaac	gcctggccgg	ccattggcgc	4560
aacctgttgc	gcggcatcgt	cgccaaaccca	cgacagcggc	tcggcgagtt	gccgctgctg	4620
gatgcgcggg	agcgccggca	gaccctctcc	gaatggaaacc	cggcccagcg	cgagtgcgcg	4680
gtgcagggca	ccttgcagca	gcgtttcgag	gagcaggcgc	ggcaacggcc	acaggcggtt	4740
gcgcgtatcc	tcgacgaaca	acggttgagc	tacggcgaac	tgaatgcgcg	ggccaatcgc	4800
ctggcgcact	gcctgatcgc	tcgcggcggtt	ggcgccgacg	tgccggtcgg	gctggcgctg	4860
gagcgttcgc	tggacatgct	ggtcggcttg	ctggcgatcc	tcaaggccgg	cggccctac	4920
ctgcccgttgg	acccggcggc	gccagaggag	cgcctggcgc	atatcctcga	cgacagtggg	4980
gtacggctgc	tgctgaccca	ggggcatctg	ctcgagcgcc	tgccgcggca	ggcgggggtg	5040
gaggtgctgg	ccatcgacgg	actggtgctg	gacggctacg	ccgagagcga	tccgctcccg	5100
acgctatcg	cggacaacct	ggcctacgtg	atctataacct	cgggctcgac	cggaagccc	5160
aagggcacgt	tgctcaccca	ccgcaacgcg	ctgcgcctgt	tcagcgccac	cgaggcctgg	5220
ttcggcttcg	acgagcggga	cgtgtggacg	ttgttccatt	cctacgcctt	cgatttctcg	5280
gtctggaaa	tcttcggcgc	gctgctctat	ggcggggcgc	tggtgatcgt	gccgcaatgg	5340
gtgagccgtt	cgccggaaaga	cttctaccgt	ctgctgtgcc	gcaaggcgt	gacggtgctc	5400
aaccagacgc	cgtcgccgtt	caagcaactg	atggcggtgg	cctgttccgc	cgacatggcg	5460
acgcagcagc	cggcgctgcg	ctacgtgate	ttcggtgccg	aggcgctggaa	tctgcagagc	5520
ctgcggccgt	ggttccagcg	ctttggcgat	cgccagccgc	aactggtgaa	catgtacggc	5580
atcaccgaga	ccacggtaca	cgtaacctac	cgtccggtga	gcaaggccga	cctgaagggt	5640
ggcctggtca	gtccgatcgg	cgggaccatc	ccggacctgt	cctggtacat	cctcgaccgt	5700
gacctgaacc	cggtgccgcg	cggcgccgtg	ggcgagctgt	acatcggtcg	cggccgtctg	5760
gcgccggct	acctgaggcg	gcccgggttg	agtgccaccc	gcttcgtgcc	gaacccgttc	5820
cccgccggtg	ccggcgagcg	gctgtaccgt	accggcgacc	tggcacggtt	ccaggcggat	5880

## 09743PC.ST25.txt

ggcaatatcg	agtacatcg	gcgtatcgac	caccaggtga	aggttcg	cggtatc	5940	
gaactgggtg	agatcgaagc	ggcgctcgcc	ggtctggccg	gggtacgcga	tgccgtgg	6000	
ctggcccatg	acggggtcgg	cggcacgcaa	ctggtggat	acgtggtggc	ggactcggcg	6060	
gaggatgccg	agcgtctg	cg	ggagtcgctg	cg	ggagtcgc	6120	
tacatggtgc	cg	ggcgcac	ct	gatgtgc	gagcggatgc	6180	
ctcgaccggc	aggcg	ttg	cc	gatgtgc	cg	gacgg	6240
cccggttagcg	agctggagca	gcgc	atcg	gc	gatctgg	6300	
cggtcg	gg	tt	gg	gg	atc	ctt	6360
ctcaaggagc	ggatcggc	ga	tac	gtc	gatc	ggc	6420
catgccagcg	tcg	cg	gg	gg	atc	ggc	6480
gtgccc	ctca	acgg	cagg	cg	cg	ttc	6540
tctgtcact	gttaca	agg	ac	atc	cg	ttc	6600
gttgc	gt	cc	ct	gt	gg	ttc	6660
gcggaata	cc	gag	ca	tt	gt	gg	6720
tgg	tc	cg	ct	cg	gg	gg	6780
cagg	tc	gt	cg	cc	gg	gg	6840
aac	gag	at	cg	cc	gg	gg	6900
gaact	gt	tc	at	cg	gg	gg	6960
atct	gt	ct	cc	cc	gg	gg	7020
gcgg	ag	at	cg	gg	gg	gg	7080
gaagt	gt	tc	cct	gg	gg	gg	7140
cgt	tc	ac	gg	gg	gg	gg	7200
agc	gc	gg	gt	gg	gg	gg	7260
gtg	ct	gg	ata	cc	cc	cc	7320
gcc	cc	ct	gg	gg	gg	gg	7347

<210> 18  
 <211> 2448  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*

<400> 18

Met Gln Ala Leu Ile Glu Lys Val Gly Ser Leu Ser Pro Gln Glu Arg  
 1 5 10 15

Lys Ala Leu Ala Val Leu Leu Lys Gln Gln Gly Val Asn Leu Phe Glu  
 Page 22

20

09743PC.ST25.txt

25

30

Ile Ala Pro Val Phe Lys Arg Gln Asp Gly Glu Pro Leu Arg Leu Ser  
35 40 45

Tyr Ala Gln Glu Arg Gln Trp Phe Leu Trp Gln Leu Glu Pro Glu Ser  
50 55 60

Ala Ala Tyr His Ile Pro Ser Val Leu Arg Leu Arg Gly Arg Leu Asp  
65 70 75 80

Leu Asp Ala Leu Gln Arg Ser Phe Asp Ser' Leu Val Ala Arg His Glu  
85 90 95

Thr Leu Arg Thr Arg Phe Arg Leu Asp Gly Asp Glu Ala Arg Gln Glu  
100 105 110

Ile Ala Ala Ser Met Ala Leu Pro Leu Asp Ile Val Ala Leu Gly Pro  
115 120 125

Leu Glu Glu Gly Ala Leu Ala Arg Gln Val Glu Thr Thr Ile Ala Arg  
130 135 140

Pro Phe Asp Leu Glu Arg Gly Pro Leu Leu Arg Val Ser Leu Leu Arg  
145 150 155 160

Leu Ala Glu Asp Asp His Val Leu Val Leu Val Gln His His Ile Val  
165 170 175

Ser Asp Gly Trp Ser Met Gln Val Met Val Glu Glu Leu Val Gln Leu  
180 185 190

Tyr Ala Ala Tyr Ser Arg Gly Leu Glu Val Ala Leu Pro Ala Leu Pro  
195 200 205

Ile Gln Tyr Ala Asp Tyr Ala Leu Trp Gln Arg Ser Trp Met Glu Ala  
210 215 220

Gly Glu Lys Glu Arg Gln Leu Ala Tyr Trp Thr Gly Leu Leu Gly Gly  
225 230 235 240

Glu Gln Pro Val Leu Glu Leu Pro Phe Asp Arg Pro Arg Pro Val Arg  
245 250 255

Gln Ser His Arg Gly Ala Gln Phe Ile Leu Glu Leu Asp Ile Asp Leu  
260 265 270

Ser Gln Ala Leu Arg Arg Val Ala Gln Gln Glu Gly Ala Thr Ala Phe  
Page 23

275

280

285

09743PC.ST25.txt

Ala Leu Leu Leu Ala Ser Phe Gln Ala Leu Leu Tyr Arg Tyr Ser Gly  
290 295 300

Gln Ala Asp Ile Arg Val Gly Val Pro Ile Ala Asn Arg Asn Arg Val  
305 310 315 320

Glu Thr Glu Arg Leu Ile Gly Phe Phe Val Asn Thr Gln Val Leu Lys  
325 330 335

Ala Asp Leu Asp Gly Arg Met Gly Phe Asp' Glu Leu Leu Ala Gln Ala  
340 345 350

Arg Gln Arg Ala Leu Glu Ala Gln Ala His Gln Asp Leu Pro Phe Glu  
355 360 365

Gln Leu Val Glu Ala Leu Gln Pro Glu Arg Ser Leu Ser His Asn Pro  
370 375 380

Leu Phe Gln Val Leu Phe Asn Tyr Gln Ser Glu Ala Arg Gly Asn Gly  
385 390 395 400

Gln Ala Phe Arg Phe Asp Glu Leu Gln Met Glu Ser Val Gln Phe Asp  
405 410 415

Ser Arg Thr Ala Gln Phe Asp Leu Thr Leu Asp Leu Thr Asp Glu Glu  
420 425 430

Gln Arg Phe Cys Ala Val Phe Asp Tyr Ala Thr Asp Leu Phe Asp Ala  
435 440 445

Ser Thr Val Glu Arg Leu Ala Gly His Trp Arg Asn Leu Leu Arg Gly  
450 455 460

Ile Val Ala Asn Pro Arg Gln Arg Leu Gly Glu Leu Pro Leu Leu Asp  
465 470 475 480

Ala Pro Glu Arg Arg Gln Thr Leu Ser Glu Trp Asn Pro Ala Gln Arg  
485 490 495

Glu Cys Ala Val Gln Gly Thr Leu Gln Gln Arg Phe Glu Glu Gln Ala  
500 505 510

Arg Gln Arg Pro Gln Ala Val Ala Leu Ile Leu Asp Glu Gln Arg Leu  
515 520 525

Ser Tyr Gly Glu Leu Asn Ala Arg Ala Asn Arg Leu Ala His Cys Leu  
Page 24

530

535

09743PC.ST25.txt

540

Ile Ala Arg Gly Val Gly Ala Asp Val Pro Val Gly Leu Ala Leu Glu  
545 550 555 560

Arg Ser Leu Asp Met Leu Val Gly Leu Leu Ala Ile Leu Lys Ala Gly  
565 570 575

Gly Ala Tyr Leu Pro Leu Asp Pro Ala Ala Pro Glu Glu Arg Leu Ala  
580 585 590

His Ile Leu Asp Asp Ser Gly Val Arg Leu Leu Leu Thr Gln Gly His  
595 600 605

Leu Leu Glu Arg Leu Pro Arg Gln Ala Gly Val Glu Val Leu Ala Ile  
610 615 620

Asp Gly Leu Val Leu Asp Gly Tyr Ala Glu Ser Asp Pro Leu Pro Thr  
625 630 635 640

Leu Ser Ala Asp Asn Leu Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr  
645 650 655

Gly Lys Pro Lys Gly Thr Leu Leu Thr His Arg Asn Ala Leu Arg Leu  
660 665 670

Phe Ser Ala Thr Glu Ala Trp Phe Gly Phe Asp Glu Arg Asp Val Trp  
675 680 685

Thr Leu Phe His Ser Tyr Ala Phe Asp Phe Ser Val Trp Glu Ile Phe  
690 695 700

Gly Ala Leu Leu Tyr Gly Gly Cys Leu Val Ile Val Pro Gln Trp Val  
705 710 715 720

Ser Arg Ser Pro Glu Asp Phe Tyr Arg Leu Leu Cys Arg Glu Gly Val  
725 730 735

Thr Val Leu Asn Gln Thr Pro Ser Ala Phe Lys Gln Leu Met Ala Val  
740 745 750

Ala Cys Ser Ala Asp Met Ala Thr Gln Gln Pro Ala Leu Arg Tyr Val  
755 760 765

Ile Phe Gly Gly Glu Ala Leu Asp Leu Gln Ser Leu Arg Pro Trp Phe  
770 775 780

Gln Arg Phe Gly Asp Arg Gln Pro Gln Leu Val Asn Met Tyr Gly Ile  
Page 25

09743PC.ST25.txt

785 790 795 800

Thr Glu Thr Thr Val His Val Thr Tyr Arg Pro Val Ser Glu Ala Asp  
805 810 815

Leu Glu Gly Gly Leu Val Ser Pro Ile Gly Gly Thr Ile Pro Asp Leu  
820 825 830

Ser Trp Tyr Ile Leu Asp Arg Asp Leu Asn Pro Val Pro Arg Gly Ala  
835 840 845

Val Gly Glu Leu Tyr Ile Gly Arg Ala Gly Leu Ala Arg Gly Tyr Leu  
850 855 860

Arg Arg Pro Gly Leu Ser Ala Thr Arg Phe Val Pro Asn Pro Phe Pro  
865 870 875 880

Gly Gly Ala Gly Glu Arg Leu Tyr Arg Thr Gly Asp Leu Ala Arg Phe  
885 890 895

Gln Ala Asp Gly Asn Ile Glu Tyr Ile Gly Arg Ile Asp His Gln Val  
900 905 910

Lys Val Arg Gly Phe Arg Ile Glu Leu Gly Glu Ile Glu Ala Ala Leu  
915 920 925

Ala Gly Leu Ala Gly Val Arg Asp Ala Val Val Leu Ala His Asp Gly  
930 935 940

Val Gly Gly Thr Gln Leu Val Gly Tyr Val Val Ala Asp Ser Ala Glu  
945 950 955 960

Asp Ala Glu Arg Leu Arg Glu Ser Leu Arg Glu Ser Leu Lys Arg His  
965 970 975

Leu Pro Asp Tyr Met Val Pro Ala His Leu Met Leu Leu Glu Arg Met  
980 985 990

Pro Leu Thr Val Asn Gly Lys Leu Asp Arg Gln Ala Leu Pro Gln Pro  
995 1000 1005

Asp Ala Ser Leu Ser Gln Gln Ala Tyr Arg Ala Pro Gly Ser Glu  
1010 1015 1020

Leu Glu Gln Arg Ile Ala Ala Ile Trp Ser Glu Ile Leu Gly Val  
1025 1030 1035

Glu Arg Val Gly Leu Asp Asp Asn Phe Phe Glu Leu Gly Gly His

1040

1045

09743PC.ST25.txt

1050

Ser Leu Leu Ala Thr Arg Val Ile Ser Arg Val Arg Gln Glu Gln  
1055 1060 1065

Gln Leu Asp Ala Ser Leu Lys Ala Leu Phe Glu Arg Pro Val Leu  
1070 1075 1080

Glu Ala Phe Ala Gln Gly Leu Glu Arg Thr Thr Asp Ala Val Ser  
1085 1090 1095

Thr Ile Pro Leu Ala Asp Arg Gln Gln Pro Leu Ala Leu Ser Phe  
1100 1105 1110

Ala Gln Glu Arg Gln Trp Phe Leu Trp Gln Leu Glu Pro Glu Ser  
1115 1120 1125

Ala Ala Tyr His Ile Pro Ser Ala Leu Arg Leu Arg Gly Arg Leu  
1130 1135 1140

Asp Val Asp Ala Leu Gln Arg Ser Phe Asp Ser Leu Val Ala Arg  
1145 1150 1155

His Glu Thr Leu Arg Thr Arg Phe Arg Leu Glu Gly Gly Arg Ser  
1160 1165 1170

Tyr Gln Gln Val Gln Pro Ala Val Ser Val Ser Ile Glu Arg Glu  
1175 1180 1185

Gln Phe Gly Glu Glu Gly Leu Ile Glu Arg Ile Gln Ala Ile Val  
1190 1195 1200

Val Gln Pro Phe Asp Leu Glu Arg Gly Pro Leu Leu Arg Val Asn  
1205 1210 1215

Leu Leu Gln Leu Ala Glu Asp Asp His Val Leu Val Leu Val Gln  
1220 1225 1230

His His Ile Val Ser Asp Gly Trp Ser Met Gln Val Met Val Glu  
1235 1240 1245

Glu Leu Val Gln Leu Tyr Ala Ala Tyr Ser Gln Gly Leu Asp Val  
1250 1255 1260

Val Leu Pro Ala Leu Pro Ile Gln Tyr Ala Asp Tyr Ala Leu Trp  
1265 1270 1275

Gln Arg Ser Trp Met Glu Ala Gly Glu Lys Glu Arg Gln Leu Ala  
Page 27

## 09743PC.ST25.txt

1280

1285

1290

Tyr Trp Thr Gly Leu Leu Gly Gly Glu Gln Pro Val Leu Glu Leu  
1295 1300 1305

Pro Phe Asp Arg Pro Arg Pro Ala Arg Gln Ser His Arg Gly Ala  
1310 1315 1320

Gln Leu Gly Phe Glu Leu Ser Arg Glu Leu Val Glu Ala Val Arg  
1325 1330 1335

Ala Leu Ala Gln Arg Glu Gly Ala Ser Ser Phe Met Leu Leu Leu  
1340 1345 1350

Ala Ser Phe Gln Ala Leu Leu Tyr Arg Tyr Ser Gly Gln Ala Asp  
1355 1360 1365

Ile Arg Val Gly Val Pro Ile Ala Asn Arg Asn Arg Val Glu Thr  
1370 1375 1380

Glu Arg Leu Ile Gly Phe Phe Val Asn Thr Gln Val Leu Lys Ala  
1385 1390 1395

Asp Leu Asp Gly Arg Met Gly Phe Asp Glu Leu Leu Ala Gln Ala  
1400 1405 1410

Arg Gln Arg Ala Leu Glu Ala Gln Ala His Gln Asp Leu Pro Phe  
1415 1420 1425

Glu Gln Leu Val Glu Ala Leu Gln Pro Glu Arg Asn Ala Ser His  
1430 1435 1440

Asn Pro Leu Phe Gln Val Leu Phe Asn His Gln Ser Glu Ile Arg  
1445 1450 1455

Ser Val Thr Pro Glu Val Gln Leu Glu Asp Leu Arg Leu Glu Gly  
1460 1465 1470

Leu Ala Trp Asp Gly Gln Thr Ala Gln Phe Asp Leu Thr Leu Asp  
1475 1480 1485

Ile Gln Glu Asp Glu Asn Gly Ile Trp Ala Ser Phe Asp Tyr Ala  
1490 1495 1500

Thr Asp Leu Phe Asp Ala Ser Thr Val Glu Arg Leu Ala Gly His  
1505 1510 1515

Trp Arg Asn Leu Leu Arg Gly Ile Val Ala Asn Pro Arg Gln Arg

1520

1525

1530

09743PC.ST25.txt

Leu Gly Glu Leu Pro Leu Leu Asp Ala Pro Glu Arg Arg Gln Thr  
1535 1540 1545

Leu Ser Glu Trp Asn Pro Ala Gln Arg Glu Cys Ala Val Gln Gly  
1550 1555 1560

Thr Leu Gln Gln Arg Phe Glu Glu Gln Ala Arg Gln Arg Pro Gln  
1565 1570 1575

Ala Val Ala Leu Ile Leu Asp Glu Gln Arg Leu Ser Tyr Gly Glu  
1580 1585 1590

Leu Asn Ala Arg Ala Asn Arg Leu Ala His Cys Leu Ile Ala Arg  
1595 1600 1605

Gly Val Gly Ala Asp Val Pro Val Gly Leu Ala Leu Glu Arg Ser  
1610 1615 1620

Leu Asp Met Leu Val Gly Leu Leu Ala Ile Leu Lys Ala Gly Gly  
1625 1630 1635

Ala Tyr Leu Pro Leu Asp Pro Ala Ala Pro Glu Glu Arg Leu Ala  
1640 1645 1650

His Ile Leu Asp Asp Ser Gly Val Arg Leu Leu Leu Thr Gln Gly  
1655 1660 1665

His Leu Leu Glu Arg Leu Pro Arg Gln Ala Gly Val Glu Val Leu  
1670 1675 1680

Ala Ile Asp Gly Leu Val Leu Asp Gly Tyr Ala Glu Ser Asp Pro  
1685 1690 1695

Leu Pro Thr Leu Ser Ala Asp Asn Leu Ala Tyr Val Ile Tyr Thr  
1700 1705 1710

Ser Gly Ser Thr Gly Lys Pro Lys Gly Thr Leu Leu Thr His Arg  
1715 1720 1725

Asn Ala Leu Arg Leu Phe Ser Ala Thr Glu Ala Trp Phe Gly Phe  
1730 1735 1740

Asp Glu Arg Asp Val Trp Thr Leu Phe His Ser Tyr Ala Phe Asp  
1745 1750 1755

Phe Ser Val Trp Glu Ile Phe Gly Ala Leu Leu Tyr Gly Gly Arg  
Page 29

1760

1765

09743PC.ST25.txt

1770

Leu Val Ile Val Pro Gln Trp Val Ser Arg Ser Pro Glu Asp Phe  
1775 1780 1785

Tyr Arg Leu Leu Cys Arg Glu Gly Val Thr Val Leu Asn Gln Thr  
1790 1795 1800

Pro Ser Ala Phe Lys Gln Leu Met Ala Val Ala Cys Ser Ala Asp  
1805 1810 1815

Met Ala Thr Gln Gln Pro Ala Leu Arg Tyr Val Ile Phe Gly Gly  
1820 1825 1830

Glu Ala Leu Asp Leu Gln Ser Leu Arg Pro Trp Phe Gln Arg Phe  
1835 1840 1845

Gly Asp Arg Gln Pro Gln Leu Val Asn Met Tyr Gly Ile Thr Glu  
1850 1855 1860

Thr Thr Val His Val Thr Tyr Arg Pro Val Ser Glu Ala Asp Leu  
1865 1870 1875

Lys Gly Gly Leu Val Ser Pro Ile Gly Gly Thr Ile Pro Asp Leu  
1880 1885 1890

Ser Trp Tyr Ile Leu Asp Arg Asp Leu Asn Pro Val Pro Arg Gly  
1895 1900 1905

Ala Val Gly Glu Leu Tyr Ile Gly Arg Ala Gly Leu Ala Arg Gly  
1910 1915 1920

Tyr Leu Arg Arg Pro Gly Leu Ser Ala Thr Arg Phe Val Pro Asn  
1925 1930 1935

Pro Phe Pro Gly Gly Ala Gly Glu Arg Leu Tyr Arg Thr Gly Asp  
1940 1945 1950

Leu Ala Arg Phe Gln Ala Asp Gly Asn Ile Glu Tyr Ile Gly Arg  
1955 1960 1965

Ile Asp His Gln Val Lys Val Arg Gly Phe Arg Ile Glu Leu Gly  
1970 1975 1980

Glu Ile Glu Ala Ala Leu Ala Gly Leu Ala Gly Val Arg Asp Ala  
1985 1990 1995

Val Val Leu Ala His Asp Gly Val Gly Gly Thr Gln Leu Val Gly  
Page 30

2000

2005

09743PC.ST25.txt

2010

Tyr Val Val Ala Asp Ser Ala Glu Asp Ala Glu Arg Leu Arg Glu  
2015 2020 2025

Ser Leu Arg Glu Ser Leu Lys Arg His Leu Pro Asp Tyr Met Val  
2030 2035 2040

Pro Ala His Leu Met Leu Leu Glu Arg Met Pro Leu Thr Val Asn  
2045 2050 2055

Gly Lys Leu Asp Arg Gln Ala Leu Pro Gln Pro Asp Ala Ser Leu  
2060 2065 2070

Ser Gln Gln Ala Tyr Arg Ala Pro Gly Ser Glu Leu Glu Gln Arg  
2075 2080 2085

Ile Ala Ala Ile Trp Ala Glu Ile Leu Gly Val Glu Arg Val Gly  
2090 2095 2100

Leu Asp Asp Asn Phe Phe Glu Leu Gly Gly His Ser Leu Leu Leu  
2105 2110 2115

Leu Met Leu Lys Glu Arg Ile Gly Asp Thr Cys Gln Ala Thr Leu  
2120 2125 2130

Ser Ile Ser Gln Leu Met Thr His Ala Ser Val Ala Glu Gln Ala  
2135 2140 2145

Ala Cys Ile Glu Gly Gln Ala Arg Glu Ser Leu Leu Val Pro Leu  
2150 2155 2160

Asn Gly Arg Arg Glu Gly Ser Pro Leu Phe Met Phe His Pro Ser  
2165 2170 2175

Phe Gly Ser Val His Cys Tyr Lys Thr Leu Ala Met Ala Leu Arg  
2180 2185 2190

Asp Arg His Pro Val Lys Gly Val Val Cys Arg Ala Leu Leu Gly  
2195 2200 2205

Ala Gly Arg Glu Val Pro Glu Trp Asp Asp Met Val Ala Glu Tyr  
2210 2215 2220

Ala Glu Gln Leu Leu Gln Glu His Pro Glu Gly Val Phe Asn Leu  
2225 2230 2235

Ala Gly Trp Ser Leu Gly Gly Asn Leu Ala Met Asp Val Ala Ala  
Page 31

2240

2245

2250

09743PC.ST25.txt

Arg Leu Glu Gln Arg Gly Arg Gln Val Ala Phe Val Gly Trp Ile  
 2255 2260 2265

Asp Ala Pro Ala Pro Val Arg Val Glu Ala Phe Trp Asn Glu Ile  
 2270 2275 2280

Gly Pro Thr Pro Glu Ala Val Pro Asn Leu Ser Val Gly Glu Met  
 2285 2290 2295

Arg Val Glu Leu Leu Gly Val Met Phe Pro Glu Arg Ala Glu His  
 2300 2305 2310

Ile Glu Arg Ala Trp Ser Ser Ile Cys Ser Ala Thr Thr Asp Asp  
 2315 2320 2325

Glu Gln Arg Trp Thr Arg Met Ser Asp Trp Ala Glu Ala Glu Ile  
 2330 2335 2340

Gly Ala Glu Phe Ala Thr Leu Arg Ser Glu Ile Ala Gln Ser Asn  
 2345 2350 2355

Glu Leu Glu Val Ser Trp Glu Leu Lys Gln Ile Leu Asp Glu Arg  
 2360 2365 2370

Leu Lys Ala Met Asp Tyr Pro Arg Leu Thr Ala Lys Val Ser Leu  
 2375 2380 2385

Trp Trp Ala Ala Arg Ser Thr Asn Ala Ile Gln Arg Ser Ala Val  
 2390 2395 2400

Glu Arg Ser Met Ala Glu Ala Ile Gly Ala Glu Arg Val Glu Pro  
 2405 2410 2415

Val Arg Val Leu Asp Thr Arg His Asp Lys Ile Ile Asp His Pro  
 2420 2425 2430

Glu Phe Val Gln Ser Phe Arg Ala Ala Leu Glu Arg Ala Gly Arg  
 2435 2440 2445

&lt;210&gt; 19

&lt;211&gt; 3132

&lt;212&gt; DNA

&lt;213&gt; Pseudomonas aeruginosa

&lt;400&gt; 19

atgtccgaat tcttcatcaa gcggccgaac ttgcgcctggg tggtggccct gttcatctcc 60

ctggccggcc tgctggtcat ttccaaattg ccggtagcgc agtaccccaa tgtcgcccg 120

## 09743PC.ST25.txt

ccacagatca	ccatcaccgc	cacctatccc	ggcgccctcg	cgaagggtgct	ggtgga	ctcc	180
gtcaccagt	tgctcgagga	gtcgctgaac	ggcgccaagg	gcctgctcta	cttcgagtcg		240
accaacaact	ccaacggcac	cgccgagatc	gtcgtcacct	tcgagccggg	caccgatccg		300
gacctggccc	aggtggacgt	gcagaaccgc	ctgaagaaag	ccgaggcgcg	catgcccgcag		360
gcggtgctga	cccagggcct	gcaggtcgag	cagaccagcg	ccggtttcct	gctgatctat		420
gcgctcagct	acaaggaagg	cgctcagcgc	agcgacacca	ccgcctcg	cgactacgccc		480
gcgcgcaata	tcaacaacga	gctgcggcgc	ctgcccggcg	tcggcaagct	gcaatttttc		540
tcttcggagg	cggccatgcg	ggtctggatc	gatccgcaga	agctggtggg	cttcggcctc		600
tccatcgacg	acgtgagcaa	tgccatccgc	gggcagaacg	tgcaagg	tgccggcgcc		660
ttcggcagcg	caccggcag	ttccgcgcag	gagctgacgg	cgaccctggc	ggtgaagg		720
accctggacg	atccgcagga	gttcggccag	gtatgtctgc	gcccacacg	ggacggctcg		780
ctgggtccggc	tcgcccgtgt	cgcgcgcctg	gaactcggca	aggagagcta	caacattttc		840
tcgcgactga	acggcacgccc	caccgtggc	ggggctatcc	agctgtcgcc	cggggccaac		900
gcgatccaga	ccgctaccct	ggtgaaacag	cgtctcgccg	aactgtcgcc	gttcttcccc		960
gaggacatgc	agtacagcgt	gccctacgac	acctcgct	tcgtcgacgt	ggccatcgag		1020
aaggtgatcc	acaccctgat	cgaagcgat	gtcctgggt	tcctgggtat	gttccctgttc		1080
ctgcagaacg	tccgctacac	cctgatcccg	tccatcg	tgccgggtgt	cctgctgggt		1140
acgctgatgg	tgtatgtacct	gctgggtt	tcggtaaca	tgtgaccat	gttcggcat		1200
gtcctggcga	tcggcatcct	ggtggacgac	gccatcg	tgg	cgagcgg		1260
atcatggcgg	aggagggat	ttcccccggcc	gaggccacgg	tcaaggcgat	gaagcaggta		1320
tccggcgcca	tcgtcgcat	caccctgg	ctctcg	tgttcc	ctgc	gcttc	1380
atggccgg	cggtgggggt	gatctaccag	cagttctcg	tgtcg	ctggc	ggtc	1440
ctgttctccg	gttccctcg	cctgac	cccccggc	tgtcg	ccac	gctg	1500
cccattcccg	aagggcacca	cgagaagcgc	ggcttctcg	gccc	ttcaa	ccgtgg	1560
gcccgcgtca	ccgagcgcta	ttcgctg	aactcg	tgg	ggcgc	cgccgg	1620
ttcatcg	ttgtacgccc	cctgg	ttgg	tcgac	gtgca	actg	1680
gaagc	ttcg	ttcg	ttgg	tcgac	gtgca	actg	1740
ggcg	cttc	cg	gggg	tcg	ggc	cttc	1800
cg	cg	cg	gggg	tcg	ggc	cttc	1860
aatg	ccgc	ccgc	ttcc	tcgg	ggct	ccagg	1920
gccc	ccgc	ccgc	ttcc	tcgg	ggct	ccagg	1980
atggcc	cgcc	ccacc	gatca	acgg	ttcc	ccgg	2040

## 09743PC.ST25.txt

ctgatggacc	gtagccccgt	cgcccgcgaa	gcgcgtgc	aggctcgca	tactcttctt	2100
ggcgagatcc	agaccaaccc	gaaattcctt	tacgcgatga	tggaaggact	ggccgaagcg	2160
ccgcaactgc	gcctgttgc	cgaccggag	aaggcccgtg	ccctgggggt	gagcttcgag	2220
accatcagcg	gcacgctgtc	cgctgccttc	ggctcggagg	tgatcaacga	cttcaccaat	2280
gcggggcgcc	aacagccccgt	ggtgatccag	gccgaacagg	gcaaccggat	gaccccgaa	2340
agcgtgctcg	agctatacgt	gcctaacgct	gctggcaacc	tggtaccgct	cagcgccttc	2400
gtcagcgtga	aatggaaaga	gggaccgggt	caattggtgc	gctataacgg	ctacccgtcg	2460
atccgcacatcg	tcggtgacgc	cgcgccccggc	ttcagtaccg	gcgaagccat	ggcggaaatg	2520
gagcgcctgg	cctcgcagct	gccggccggc	atcggctacg	agtggaccgg	cctgtcctat	2580
caggagaagg	tctccgcgg	gcaggccacc	agcctgttgc	ccctcgccat	cctgggtgg	2640
ttcctgttgc	tggtggcgct	ctacgagagc	tggtcgatcc	cgctgtcggt	gatgctgatc	2700
gtgccgatcg	gcgcacatcg	cgcggtgctc	gcgggtatgg	tcagcggtat	gtccaaacgac	2760
gtgtatcc	aggtcggcct	gatcaccatc	atcggcttt	cggcgaagaa	cgcgatcctc	2820
atcgtcgagt	tcgccaagga	actctggag	cagggcata	gcctgcgcga	cgcgcacatc	2880
gaggccgcgc	gcctgcgcctt	ccggccgatc	atcatgactt	ccatggcggt	cattctcgcc	2940
gtgataacccc	tggccctggc	cagcggtgcc	ggcgccggcga	gccagcgtgc	catcgacc	3000
ggagtgatcg	gcgggatgct	cagcgccacc	ttcctcgccg	tgctgttgcgt	acctatctgt	3060
ttcgtctggc	tgctgtcgct	gctgcgcagc	aagccggcac	ccatcgaaca	ggccgcgttcg	3120
gccggggagt	ga					3132

&lt;210&gt; 20

&lt;211&gt; 1043

&lt;212&gt; PRT

<213> *Pseudomonas aeruginosa*

&lt;400&gt; 20

Met	Ser	Glu	Phe	Phe	Ile	Lys	Arg	Pro	Asn	Phe	Ala	Trp	Val	Val	Ala
1					5				10				15		

Leu	Phe	Ile	Ser	Leu	Ala	Gly	Leu	Leu	Val	Ile	Ser	Lys	Leu	Pro	Val
20						25				30					

Ala	Gln	Tyr	Pro	Asn	Val	Ala	Pro	Pro	Gln	Ile	Thr	Ile	Thr	Ala	Thr
35					40				45						

Tyr	Pro	Gly	Ala	Ser	Ala	Lys	Val	Leu	Val	Asp	Ser	Val	Thr	Ser	Val
50					55				60						

Leu	Glu	Glu	Ser	Leu	Asn	Gly	Ala	Lys	Gly	Leu	Leu	Tyr	Phe	Glu	Ser

65

70

09743PC.ST25.txt

75

80

Thr Asn Asn Ser Asn Gly Thr Ala Glu Ile Val Val Thr Phe Glu Pro  
85 90 95

Gly Thr Asp Pro Asp Leu Ala Gln Val Asp Val Gln Asn Arg Leu Lys  
100 105 110

Lys Ala Glu Ala Arg Met Pro Gln Ala Val Leu Thr Gln Gly Leu Gln  
115 120 125

Val Glu Gln Thr Ser Ala Gly Phe Leu Leu Ile Tyr Ala Leu Ser Tyr  
130 135 140

Lys Glu Gly Ala Gln Arg Ser Asp Thr Thr Ala Leu Gly Asp Tyr Ala  
145 150 155 160

Ala Arg Asn Ile Asn Asn Glu Leu Arg Arg Leu Pro Gly Val Gly Lys  
165 170 175

Leu Gln Phe Phe Ser Ser Glu Ala Ala Met Arg Val Trp Ile Asp Pro  
180 185 190

Gln Lys Leu Val Gly Phe Gly Leu Ser Ile Asp Asp Val Ser Asn Ala  
195 200 205

Ile Arg Gly Gln Asn Val Gln Val Pro Ala Gly Ala Phe Gly Ser Ala  
210 215 220

Pro Gly Ser Ser Ala Gln Glu Leu Thr Ala Thr Leu Ala Val Lys Gly  
225 230 235 240

Thr Leu Asp Asp Pro Gln Glu Phe Gly Gln Val Val Leu Arg Ala Asn  
245 250 255

Glu Asp Gly Ser Leu Val Arg Leu Ala Asp Val Ala Arg Leu Glu Leu  
260 265 270

Gly Lys Glu Ser Tyr Asn Ile Ser Ser Arg Leu Asn Gly Thr Pro Thr  
275 280 285

Val Gly Gly Ala Ile Gln Leu Ser Pro Gly Ala Asn Ala Ile Gln Thr  
290 295 300

Ala Thr Leu Val Lys Gln Arg Leu Ala Glu Leu Ser Ala Phe Phe Pro  
305 310 315 320

Glu Asp Met Gln Tyr Ser Val Pro Tyr Asp Thr Ser Arg Phe Val Asp  
Page 35

09743PC.ST25.txt  
325 330 335

Val Ala Ile Glu Lys Val Ile His Thr Leu Ile Glu Ala Met Val Leu  
340 345 350

Val Phe Leu Val Met Phe Leu Phe Leu 'Gln Asn Val Arg Tyr Thr Leu  
355 360 365

Ile Pro Ser Ile Val Val Pro Val Cys Leu Leu Gly Thr Leu Met Val  
370 375 380

Met Tyr Leu Leu Gly Phe Ser Val Asn Met Met Thr Met Phe Gly Met  
 385 390 395 400

Val Leu Ala Ile Gly Ile Leu Val Asp Asp Ala Ile Val Val Val Glu  
405 410 415

Asn Val Glu Arg Ile Met Ala Glu Glu Gly Ile Ser Pro Ala Glu Ala  
420 425 430

Thr Val Lys Ala Met Lys Gln Val Ser Gly Ala Ile Val Gly Ile Thr  
435 440 445

Leu Val Leu Ser Ala Val Phe Leu Pro. Leu Ala Phe Met Ala Gly Ser  
450 455 460

Val Gly Val Ile Tyr Gln Gln Phe Ser Val Ser Leu Ala Val Ser Ile  
465 470 475 480

Leu Phe Ser Gly Phe Leu Ala Leu Thr Phe Thr Pro Ala Leu Cys Ala  
485 490 495

Thr Leu Leu Lys Pro Ile Pro Glu Gly His His Glu Lys Arg Gly Phe  
500 505 510

Phe Gly Ala Phe Asn Arg Gly Phe Ala Arg Val Thr Glu Arg Tyr Ser  
 515 520 525

Leu Leu Asn Ser Lys Leu Val Ala Arg Ala Gly Arg Phe Met Leu Val  
530 535 540

Tyr Ala Gly Leu Val Ala Met Leu Gly Tyr Phe Tyr Leu Arg Leu Pro  
 545 550 555 560

Glu Ala Phe Val Pro Ala Glu Asp Leu Gly Tyr Met Val Val Asp Val  
565 570 575

Gln Leu Pro Pro Gly Ala Ser Arg Val Arg Thr Asp Ala Thr Gly Glu  
Page 36

580

09743PC.ST25.txt

585

590

Glu Leu Glu Arg Phe Leu Lys Ser Arg Glu Ala Val Ala Ser Val Phe  
 595 600 605

Leu Ile Ser Gly Phe Ser Phe Ser Gly Gln Gly Asp Asn Ala Ala Leu  
 610 615 620

Ala Phe Pro Thr Phe Lys Asp Trp Ser Glu Arg Gly Ala Glu Gln Ser  
 625 630 635 640

Ala Ala Ala Glu Ile Ala Ala Leu Asn Glu His Phe Ala Leu Pro Asp  
 645 650 655

Asp Gly Thr Val Met Ala Val Ser Pro Pro Pro Ile Asn Gly Leu Gly  
 660 665 670

Asn Ser Gly Gly Phe Ala Leu Arg Leu Met Asp Arg Ser Gly Val Gly  
 675 680 685

Arg Glu Ala Leu Leu Gln Ala Arg Asp Thr Leu Leu Gly Glu Ile Gln  
 690 695 700

Thr Asn Pro Lys Phe Leu Tyr Ala Met Met Glu Gly Leu Ala Glu Ala  
 705 710 715 720

Pro Gln Leu Arg Leu Leu Ile Asp Arg Glu Lys Ala Arg Ala Leu Gly  
 725 730 735

Val Ser Phe Glu Thr Ile Ser Gly Thr Leu Ser Ala Ala Phe Gly Ser  
 740 745 750

Glu Val Ile Asn Asp Phe Thr Asn Ala Gly Arg Gln Gln Arg Val Val  
 755 760 765

Ile Gln Ala Glu Gln Gly Asn Arg Met Thr Pro Glu Ser Val Leu Glu  
 770 775 780

Leu Tyr Val Pro Asn Ala Ala Gly Asn Leu Val Pro Leu Ser Ala Phe  
 785 790 795 800

Val Ser Val Lys Trp Glu Glu Gly Pro Val Gln Leu Val Arg Tyr Asn  
 805 810 815

Gly Tyr Pro Ser Ile Arg Ile Val Gly Asp Ala Ala Pro Gly Phe Ser  
 820 825 830

Thr Gly Glu Ala Met Ala Glu Met Glu Arg Leu Ala Ser Gln Leu Pro  
 Page 37

835

840

845

09743PC.ST25.txt

Ala Gly Ile Gly Tyr Glu Trp Thr Gly Leu Ser Tyr Gln Glu Lys Val  
 850 855 860

Ser Ala Gly Gln Ala Thr Ser Leu Phe Ala Leu Ala Ile Leu Val Val  
 865 870 875 880

Phe Leu Leu Leu Val Ala Leu Tyr Glu Ser Trp Ser Ile Pro Leu Ser  
 885 890 895

Val Met Leu Ile Val Pro Ile Gly Ala Ile Gly Ala Val Leu Ala Val  
 900 905 910

Met Val Ser Gly Met Ser Asn Asp Val Tyr Phe Lys Val Gly Leu Ile  
 915 920 925

Thr Ile Ile Gly Leu Ser Ala Lys Asn Ala Ile Leu Ile Val Glu Phe  
 930 935 940

Ala Lys Glu Leu Trp Glu Gln Gly His Ser Leu Arg Asp Ala Ala Ile  
 945 950 955 960

Glu Ala Ala Arg Leu Arg Phe Arg Pro Ile Ile Met Thr Ser Met Ala  
 965 970 975

Phe Ile Leu Gly Val Ile Pro Leu Ala Leu Ala Ser Gly Ala Gly Ala  
 980 985 990

Ala Ser Gln Arg Ala Ile Gly Thr Gly Val Ile Gly Gly Met Leu Ser  
 995 1000 1005

Ala Thr Phe Leu Gly Val Leu Phe Val Pro Ile Cys Phe Val Trp  
 1010 1015 1020

Leu Leu Ser Leu Leu Arg Ser Lys Pro Ala Pro Ile Glu Gln Ala  
 1025 1030 1035

Ala Ser Ala Gly Glu  
 1040

<210> 21  
 <211> 642  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 21  
 atgaacgatg cttctccccg tctgaccgaa cgccggcaggc aacgcccggc cgccatgctc 60  
 gacgccccta cccaggcctt tctcgaacac ggtttcgaag gcaccaccct ggacatggtg 120  
 Page 38

## 09743PC.ST25.txt

atagaacggg	ccggtgttgc	acgggggacc	ctgtacagct	ccttcggcgg	caaggaggc	180
ctgttcggcg	cggtgatcgc	ccacatgatc	ggggaaatct	tcgacgacag	cgccgatcag	240
ccgcgcggcg	ccgcccacgct	gagcgccacc	ctcgagcatt	tcggccggcg	ctttctcacc	300
agcctgctcg	atccccgctg	ccagagcctc	tatcgcttgg	tggtggcggg	atccccgccc	360
tttccggcga	tcggcaagtc	cttctacgag	cagggggccgc	agcagagcta	tctgctgctc	420
agcgagcgac	tggccgcggt	cgctcctcac	atggacgagg	aaacgctcta	cgcggggcc	480
tgccagtttc	tcgagatgct	caaggccgac	ctgttcctca	aggccctcag	cgtggccgac	540
ttccagccga	ccatggcgct	gctggaaacc	cgcctcaagc	tgtcggtgga	catcatcgcc	600
tgctaccttgg	aacacctgtc	gcagagcccc	gcgcagggct	ga		642

<210> 22  
 <211> 213  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*  
 <400> 22

Met Asn Asp Ala Ser Pro Arg Leu Thr Glu Arg Gly Arg Gln Arg Arg  
 1 5 10 15

Arg Ala Met Leu Asp Ala Ala Thr Gln Ala Phe Leu Glu His Gly Phe  
 20 25 30

Glu Gly Thr Thr Leu Asp Met Val Ile Glu Arg Ala Gly Gly Ser Arg  
 35 40 45

Gly Thr Leu Tyr Ser Ser Phe Gly Gly Lys Glu Gly Leu Phe Ala Ala  
 50 55 60

Val Ile Ala His Met Ile Gly Glu Ile Phe Asp Asp Ser Ala Asp Gln  
 65 70 75 80

Pro Arg Pro Ala Ala Thr Leu Ser Ala Thr Leu Glu His Phe Gly Arg  
 85 90 95

Arg Phe Leu Thr Ser Leu Leu Asp Pro Arg Cys Gln Ser Leu Tyr Arg  
 100 105 110

Leu Val Val Ala Glu Ser Pro Arg Phe Pro Ala Ile Gly Lys Ser Phe  
 115 120 125

Tyr Glu Gln Gly Pro Gln Gln Ser Tyr Leu Leu Leu Ser Glu Arg Leu  
 130 135 140

Ala Ala Val Ala Pro His Met Asp Glu Glu Thr Leu Tyr Ala Val Ala  
 Page 39

145

150

09743PC.ST25.txt

155

160

Cys Gln Phe Leu Glu Met Leu Lys Ala Asp Leu Phe Leu Lys Ala Leu  
 165 170 175

Ser Val Ala Asp Phe Gln Pro Thr Met Ala Leu Leu Glu Thr Arg Leu  
 180 185 190

Lys Leu Ser Val Asp Ile Ile Ala Cys Tyr Leu Glu His Leu Ser Gln  
 195 200 205

Ser Pro Ala Gln Gly  
 210

<210> 23  
 <211> 1017  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 23  
 atgtctgatg atgcccgtt ccagcagctg aattgctgg tggactctt gttgcccag 60  
 ttgttcgttg ccgaagggtt gggggaaagt ccccccggcc aactgatccc ggccagtagc 120  
 gacgcccagct tccgtcgtta tttccgctgg cagggagggg accgcagcct ggtggtgatg 180  
 gacgcgcccgc cgccccagga agactgccga ccgttcgtca aggtcgccgg actgctcgcc 240  
 ggagccggcg tgcatgtgcc gaggattctc gcccaggacc tggagaacgg tttcctgctg 300  
 ctcagtgacc tggggccggca gacctacctc gacgtgcttc atcccggaa tgccgacgag 360  
 ctgttcgaac cggccctggc tgcgtgatc gccttccaga aggtcgatgt cggcggtgtc 420  
 ctgcctgcct acgacgaagc ggtgctgcgc cgcgagctgc agctgttccc cgactggtagc 480  
 ctggcccgcc acctcggcgt ggagctggag ggcgagacgc tggcccgctg gaaacggatc 540  
 tgcgacactgc tggtaacgcag cgcgctggag caaccgggg tggctgtcca tcgacgtat 600  
 atgcccgcga atctgatgct cagcgagccc aaccggggcg tcctcgactt ccaggacgcc 660  
 ctgcacggcc cggtcaccta cgatgtcacc tgcctgtaca aggacgcctt cgtcagttgg 720  
 ccggagccgc gcgtgcacgc cgcgctgaac cgttactgga agaaggcgac ctggccggc 780  
 atcccgtgc cgccaagctt cgaagacttc ctccgtgcga ggcacgtat gggcggtgcag 840  
 cgccacgtga aggtgattgg catcttcgac cgtatctgtc accgcgacgg caagccgcgc 900  
 tacctgggtg acgtgcccgc cttcttccgt tatctggaaa ccggcggtggc ggcacgtccc 960  
 gagctggccg aactgggcga gctgctggcc tcgctgccc agggagccga ggcacgtat 1017

<210> 24  
 <211> 338  
 <212> PRT  
 <213> Pseudomonas aeruginosa

09743PC.ST25.txt

&lt;400&gt; 24

Met Ser Asp Asp Ala Arg Phe Gln Gln Leu Asn Cys Trp Leu Asp Ser  
1 5 10 15

Cys Leu Pro Glu Leu Phe Val Ala Glu Gly Trp Gly Glu Val Pro Pro  
20 25 30

Ala Glu Leu Ile Pro Ala Ser Ser Asp Ala Ser Phe Arg Arg Tyr Phe  
35 40 45

Arg Trp Gln Gly Gly Asp Arg Ser Leu Val Val Met Asp Ala Pro Pro  
50 55 60

Pro Gln Glu Asp Cys Arg Pro Phe Val Lys Val Ala Gly Leu Leu Ala  
65 70 75 80

Gly Ala Gly Val His Val Pro Arg Ile Leu Ala Gln Asp Leu Glu Asn  
85 90 95

Gly Phe Leu Leu Leu Ser Asp Leu Gly Arg Gln Thr Tyr Leu Asp Val  
100 105 110

Leu His Pro Gly Asn Ala Asp Glu Leu Phe Glu Pro Ala Leu Asp Ala  
115 120 125

Leu Ile Ala Phe Gln Lys Val Asp Val Ala Gly Val Leu Pro Ala Tyr  
130 135 140

Asp Glu Ala Val Leu Arg Arg Glu Leu Gln Leu Phe Pro Asp Trp Tyr  
145 150 155 160

Leu Ala Arg His Leu Gly Val Glu Leu Glu Gly Glu Thr Leu Ala Arg  
165 170 175

Trp Lys Arg Ile Cys Asp Leu Leu Val Arg Ser Ala Leu Glu Gln Pro  
180 185 190

Arg Val Phe Val His Arg Asp Tyr Met Pro Arg Asn Leu Met Leu Ser  
195 200 205

Glu Pro Asn Pro Gly Val Leu Asp Phe Gln Asp Ala Leu His Gly Pro  
210 215 220

Val Thr Tyr Asp Val Thr Cys Leu Tyr Lys Asp Ala Phe Val Ser Trp  
225 230 235 240

Pro Glu Pro Arg Val His Ala Ala Leu Asn Arg Tyr Trp Lys Lys Ala  
Page 41

245

09743PC.ST25.txt

250

255

Thr Trp Ala Gly Ile Pro Leu Pro Pro Ser Phe Glu Asp Phe Leu Arg  
 260 265 270

Ala Ser Asp Leu Met Gly Val Gln Arg His Leu Lys Val Ile Gly Ile  
 275 280 285

Phe Ala Arg Ile Cys His Arg Asp Gly Lys Pro Arg Tyr Leu Gly Asp  
 290 295 300

Val Pro Arg Phe Phe Arg Tyr Leu Glu Thr Ala Val Ala Arg Arg Pro  
 305 310 315 320

Glu Leu Ala Glu Leu Gly Glu Leu Leu Ala Ser Leu Pro Gln Gly Ala  
 325 330 335

Glu Ala

<210> 25  
 <211> 3270  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 25  
 atgagcggat tccaggacca gagtatcgac gaaggcgtgc gcaagcgcac cgcctaccag 60  
 aacgatcggc gtgcacgact ggcattgaac gtcgagcgcac aggacggcgg tattcctgcag 120  
 attccggtgg ccagcgatat gctcggccat gaggagcacg agcgtatcca gcagaacacc 180  
 ttcctggctg ttagtgcgcgt ggtccgcctg ccaacgctgg gcaaggccgg ttatggcgcac 240  
 cagctgcccgg cccgcgcgt accgcgggacg ggacggatct acctgttcca ggacggcaag 300  
 ttgtggcgcg aacttggaaatg ttagtggcaag ggcaacctgt tcgaagtcga tctcctgcag 360  
 gggcgcagcc agcgtgcggc caagcgtccg gccttaggca agacacaagc gctgatcctg 420  
 gtgcccggcgtc tggtaagggg gcagttcgtg atcccacgct acaccatggc ctatagcgaa 480  
 actccctggc cttggtcgtt catcgactgg ctggaggagg acccgcagcg ggtcaaccgg 540  
 cgctgcccagc agatggcgtc cgcttggaaac gcctcggtgg ccaaccagca ctggaaagcc 600  
 tccatccatc aaccgcgcgt ggtcattgtat catcacgccc agggtttgcg acctcgccgac 660  
 ttcaacgtcg agagcgcgcgt ggaagacccg gcggaaattca cacctgagtt cgccgcctt 720  
 cgcgaagagt cgctgggtgtc ccagttgcag cgacgccagc aggaattggc gcccctgctg 780  
 aagcaggctc cgccctctgc gctacctact ctggaaagccg gagaggacgt actggaaacc 840  
 ctcaagctgc gtggccatcc caacccatc gggctgatgc tcgacgactc gctgttcgccc 900  
 ttgcggccacg ctgcggcgcac ggcgcgcac tgcggccctt acttgcgcag cctcaatgca 960

## 09743PC.ST25.txt

ctgctgccgc accgtcccaa	1020
ccgctcgcca agctcagggg	1080
gaggagcgac agtcttgcgg	1140
ctggaaggcc ccttgcaccc	1200
ctggagccct acagcctgat	1260
tgcgacgcac tgtacagcgg	1320
gtcagcacgg ttctgcaggc	1380
ggacaacttc ccgagccggt	1440
gaccccgatg caatgggcct	1500
gaccagccca gcgccggcaa	1560
ggcgccagcg tagtcgagca	1620
gaccgcttgc tgcgaccgac	1680
atccgcctgc tgcccgcacag	1740
gcccgcctgc gcaacggtct	1800
ccggccgcca tcgttcagga	1860
accggcatga gtcgcgccaa	1920
ccggacctgc ttgcctacac	1980
gagaacactc gcacgtgccc	2040
caggtgcagg catacagtgg	2100
gctgtcggtg cagtaatcga	2160
ggaccatcta ctgcaaagta	2220
cgtatggcca ggaatctaga	2280
cttgggtggcg cagccacact	2340
ttgaggcagg gagatagcga	2400
ctttgggttg cctacgtcct	2460
gttttggcga tcggaggcac	2520
atcgtaaaga aaggcccatt	2580
atggggcagg accagcgctt	2640
ctgggagtcc tcggccatcc	2700
gcccgcgg cgcacatcgatc	2760
cgcactgcgc tatcctgcat	2820
gtggtgctga gttcccccgt	2880

## 09743PC.ST25.txt

gtggcccaagg	agtttctcag	cagcttgcgg	atcgatccgg	gcaccctgtt	cggcgtcaag	2940
cgctaccatc	gggtccccgc	gggccccgccc	aagctcgaag	ccttgcgcgtt	ggatgctgcc	3000
agcgtgctct	atgtgctgcc	ggccagcctg	ccgattccgc	agttgtctcc	tcgggccccgc	3060
tatagcatgc	gcatgaccca	gggtttgaag	atcagcgcac	agttcgaact	caatgccgac	3120
cagcctgagc	agcggcttgt	cctgcctcaa	cccagcccga	agagttggag	tgcattcaca	3180
tccgccaatc	ggtaccttcc	cccgacgac	ttggggccccc	atgctgcgcc	accttattgg	3240
ttgatagaga	acagttagtt	caacgtatga				3270

<210> 26  
 <211> 1089  
 <212> PRT  
 <213> *Pseudomonas aeruginosa*

<400> 26

Met	Ser	Gly	Phe	Gln	Asp	Gln	Ser	Ile	Asp	Glu	Gly	Val	Arg	Lys	Arg
1				5					10				15		

Thr	Ala	Tyr	Gln	Asn	Asp	Arg	Arg	Ala	Arg	Leu	Ala	Leu	Asn	Val	Glu
						20			25				30		

Arg	Gln	Asp	Gly	Gly	Ile	Leu	Gln	Ile	Pro	Val	Ala	Ser	Asp	Met	Leu
					35			40				45			

Gly	His	Glu	Glu	His	Glu	Arg	Ile	Gln	Gln	Asn	Thr	Phe	Leu	Ala	Val
					50			55			60				

Met	Pro	Leu	Val	Arg	Leu	Pro	Thr	Leu	Gly	Lys	Ala	Gly	Tyr	Gly	Asp
					65			70		75			80		

· Gln	Leu	Pro	Ala	Gly	Ala	Leu	Pro	Arg	Ala	Gly	Arg	Ile	Tyr	Leu	Phe
					85			90			95				

Gln	Asp	Gly	Lys	Leu	Trp	Arg	Glu	Leu	Glu	Cys	Asp	Gly	Lys	Gly	Asn
					100			105			110				

Leu	Phe	Glu	Val	Asp	Leu	Leu	Gln	Gly	Arg	Ser	Gln	Arg	Ala	Asp	Lys
					115			120			125				

Arg	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Ala	Leu	Ile	Leu	Val	Pro	Val	Leu
					130			135			140				

Val	Lys	Gly	Gln	Phe	Val	Ile	Pro	Arg	Tyr	Thr	Met	Ala	Tyr	Ser	Glu
					145			150			155			160	

Thr Pro Trp Pro Trp Ser Tyr Ile Asp Trp Leu Glu Glu Asp Pro Gln

165

09743PC.ST25.txt

170

175

Arg Val Asn Arg Arg Cys Gln Gln Met Ala Ser Ala Trp Asn Ala Ser  
180 185 190

Val Ala Asn Gln His Trp Lys Ala Ser Ile His Gln Pro Ala Leu Val  
195 200 205

Ile Asp His His Ala Gln Gly Leu Arg Pro Arg Asp Phe Asn Val Glu  
210 215 220

Ser Ala Leu Glu Asp Pro Ala Glu Phe Thr Pro Glu Phe Ala Ala Phe  
225 230 235 240

Arg Glu Glu Ser Leu Val Cys Gln Leu Gln Arg Arg Gln Gln Glu Leu  
245 250 255

Ala Pro Leu Leu Lys Gln Ala Pro Pro Ser Ala Leu Pro Thr Leu Glu  
260 265 270

Ala Gly Glu Asp Val Leu Glu Thr Leu Lys Leu Arg Gly His Pro Asn  
275 280 285

Leu Ile Gly Leu Met Leu Asp Asp Ser Leu Phe Ala Leu Arg His Ala  
290 295 300

Ala Ala Gln Ala Arg His Cys Ala Ala Tyr Leu Arg Ser Leu Asn Ala  
305 310 315 320

Leu Leu Pro His Arg Pro Asn Gly Arg Tyr Ala Gln Val Leu Ser Asn  
325 330 335

Met Leu Asp Gly Pro Leu Ala Lys Leu Arg Gly Glu Val Asp Gln Ala  
340 345 350

Glu Leu Asp Glu Ala Ile Phe Ala Glu Glu Arg Gln Ser Cys Arg Ile  
355 360 365

His Leu Thr Gln Gln Val Glu His Leu Val Ala Leu Leu Glu Gly Pro  
370 375 380

Leu His Pro Val Leu Gln Asp Trp Thr His Gln Cys Asp Glu Ala Leu  
385 390 395 400

Leu Glu Pro Tyr Ser Leu Met Ser Glu Ala Leu Ala Leu Asn Gln  
405 410 415

Leu Pro Asp Arg Cys Asp Ala Leu Tyr Ser Gly Thr Ala Tyr Arg Ala  
Page 45

420

09743PC.ST25.txt

425

430

Leu Ala Ala His Val Glu Arg Val Val Ser Thr Val Leu Gln Ala Ser  
435 440 445

His Pro Leu Gly Ala Met Leu Leu Ala Lys Asp Glu Gly Gln Leu Pro  
450 455 460

Glu Pro Val Arg Arg Leu Gln Ala Leu Arg Asp Ser Pro Arg Thr Pro  
465 470 475 480

Asp Pro Asp Ala Met Gly Leu Ser Thr Leu Met Leu Gly Ala Ser Leu  
485 490 495

Leu Gly Glu Val Asp Gln Pro Ser Ala Gly Lys Ser Leu Ala Tyr Phe  
500 505 510

Leu Gly Asp Leu Leu Asp Val Phe Gly Ala Ser Val Val Glu Gln Leu  
515 520 525

Gly Arg Leu Ser Gln Gly Ala Thr Gln Ile Gln Leu Asp Arg Leu Phe  
530 535 540

Ala Pro Thr Phe Asn Thr Leu Ser Ala Leu Ser Val Val Lys Met Lys Gly  
545 550 555 560

Ile Arg Leu Leu Pro Asp Ser Gln Val Pro Leu Asp Met Val Val Val  
565 570 575

Gly Val Arg Gly Ala Gly Leu Arg Asn Gly Leu Thr Glu Val Glu Arg  
580 585 590

Gln Glu Leu Arg Arg Lys Ser Tyr Arg Arg Ala Ile Val Gln Asp Gly  
595 600 605

Ala Gly Asn Pro Leu Ala Gly Thr Ser Pro Arg Asp Thr Gly Met Ser  
610 615 620

Arg Ala Asn Leu Arg Asn Val Met Val Val Ala Val Pro Lys Asp His  
625 630 635 640

Pro Asp Leu Leu Ala Tyr Thr Lys Phe Arg Thr Gln Leu Gly Thr Leu  
645 650 655

Thr Gln Val Met Glu Asn Thr Arg Ile Val Pro Thr Met Met Leu Gly  
660 665 670

Phe Ala Ile Tyr Asn Leu Asn Val Gln Val Gln Ala Tyr Ser Gly Phe  
Page 46

675 680 685  
09743PC.ST25.txtVal Asp Ser Gly Glu Lys His Arg Gly Thr Ile Gly Ala Val Gly Ala  
690 695 700Val Ile Asp Leu Thr Ala Ala Gly Gly Ser His Ala Lys Leu Leu Phe  
705 710 715 720Gly Pro Ser Thr Ala Lys Tyr Leu Glu Thr Pro Arg Ile Ser Val Ala  
725 730 735Gln Ile Ser Pro Arg Trp Ala Arg Asn Leu Glu Val Gln Thr Gly Ser  
740 745 750Pro Lys Leu Gly Leu Leu Arg Gly Leu Gly Ala Ala Thr Leu Phe  
755 760 765Gly Ala Gly Ile Ser Val Trp Asp Gly Tyr Arg Ala Leu Arg Gln Gly  
770 775 780Asp Ser Asp Ala Ala Ala Tyr Gly Val Ala Ala Val Gly Gly Gly  
785 790 795 800Leu Trp Gly Ala Tyr Val Leu Gly Trp Ile Val Asn Pro Tyr Ala Leu  
805 810 815Leu Ala Gly Ala Val Leu Ala Ile Gly Gly Thr Val Val Ala Asn Leu  
820 825 830Leu Thr Asp Ser Asp Ala Glu Thr Ile Val Lys Lys Gly Pro Phe Gly  
835 840 845Arg Gln Phe Ala Glu Ala Gly Leu Leu Asp Ser Leu Met Gly Gln Asp  
850 855 860Gln Arg Phe Ala His Leu Lys Asp Pro Gln Thr Ala Tyr Arg Gln Leu  
865 870 875 880Leu Gly Val Leu Gly His Pro Arg Val Phe Val His Arg Leu Glu Asp  
885 890 895Trp Arg Lys Leu Ala Pro Ala Ala His Arg Ser Val Leu Gln Glu Ala  
900 905 910Glu Arg Gly Arg Gln Ala Val Ser Arg Thr Ala Leu Ser Cys Ile Asp  
915 920 925Pro Lys Leu Gln Ala Leu Glu Ala Asn Asp Trp Ala Val Val Leu Ser  
Page 47

930

935

09743PC.ST25.txt

940

Ser Pro Leu Leu Ala Met Phe Glu Asn Gly Gln Lys Ala Phe Arg Leu  
 945 950 955 960

Val Ala Gln Glu Phe Leu Ser Ser Leu Pro Ile Asp Pro Gly Thr Leu  
 965 970 975

Phe Gly Val Lys Arg Tyr His Arg Val Pro Ala Gly Pro Ala Lys Leu  
 980 985 990

Glu Ala Leu Pro Leu Asp Ala Ala Ser Val Leu Tyr Val Leu Pro Ala  
 995 1000 1005

Ser Leu Pro Ile Pro Gln Leu Ser Pro Arg Ala Arg Tyr Ser Met  
 1010 1015 1020

Arg Met Thr Gln Gly Leu Lys Ile Ser Ala Gln Phe Glu Leu Asn  
 1025 1030 1035

Ala Asp Gln Pro Glu Gln Arg Leu Val Leu Pro Gln Pro Ser Pro  
 1040 1045 1050

Lys Ser Trp Ser Ala Phe Thr Ser Ala Asn Arg Tyr Leu Pro Pro  
 1055 1060 1065

Asp Asp Leu Gly Pro His Ala Ala Pro Pro Tyr Trp Leu Ile Glu  
 1070 1075 1080

Asn Ser Glu Phe Asn Val  
 1085

<210> 27  
 <211> 756  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 27  
 atgagcgtccg cctgggtccg gccgttccgc ctgacgcccga tgccgcgcct gcgcctggcc 60  
 tgcttcccccc atgcaggcgg cagcgcgcgc ttcttccgta gctggagcga acgcctgcgg 120  
 ccagacatcg acctgcttgc cctgcagtac ccgggtcgcg aggaccgcctt caacgaggcg 180  
 ccggccaccc gcctggagga cctcgccgac ggcgcgcgc tcgcgcgcgc cgatttcgcc 240  
 gacgcgcgcgc tggcgctgtt cggccacagt ctcggcgccgg cgctggccta cgaaaccgc 300  
 ctgcgcctgg aaagcgccgg cgccgcgtg cgccacgtgt tcgtctccgc ccattccggca 360  
 ccgcacccgc aacgcggcgg cgcggtgcac cgccgcgcacg aggcggcgct gctggaggac 420  
 gtccgcgcgc agggtggcgc cagcgagcta ctcgaggacg ccgacctgcg cgcgctgttc 480

## 09743PC.ST25.txt

ctggccatcc	tgcgcgccga	ctaccaggcg	atcgagacct	accgacgggc	gcagcccatc	540
gccctggcct	gcgcctcga	cgtcctcctc	ggcgagcacg	acgaggaagt	cagcggccgc	600
gaggcgccagg	cctggagcga	cgccagccgg	actcccggca	ggctgcggcg	cttcctggc	660
ggccacttct	acctgagcga	ggggcgac	gcggtgatcg	agcacctgct	gcgcccctc	720
gcacatcccc	acgcccatttc	ccgagaggtt	gcatga			756

<210> 28  
 <211> 251  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<400> 28

Met Ser Ala Ala Trp Val Arg Pro Phe Arg Leu Thr Pro Met Pro Arg  
 1 5 10 15

Leu Arg Leu Ala Cys Phe Pro His Ala Gly Gly Ser Ala Ser Phe Phe  
 20 25 30

Arg Ser Trp Ser Glu Arg Leu Pro Pro Asp Ile Asp Leu Leu Ala Leu  
 35 40 45

Gln Tyr Pro Gly Arg Glu Asp Arg Phe Asn Glu Ala Pro Ala Thr Arg  
 50 55 60

Leu Glu Asp Leu Ala Asp Gly Ala Ala Leu Ala Leu Arg Asp Phe Ala  
 65 70 75 80

Asp Ala Pro Leu Ala Leu Phe Gly His Ser Leu Gly Ala Ala Leu Ala  
 85 90 95

Tyr Glu Thr Ala Leu Arg Leu Glu Ser Ala Gly Ala Pro Leu Arg His  
 100 105 110

Leu Phe Val Ser Ala His Pro Ala Pro His Arg Gln Arg Gly Gly Ala  
 115 120 125

Leu His Arg Gly Asp Glu Ala Ala Leu Leu Glu Asp Val Arg Arg Gln  
 130 135 140

Gly Gly Ala Ser Glu Leu Leu Glu Asp Ala Asp Leu Arg Ala Leu Phe  
 145 150 155 160

Leu Pro Ile Leu Arg Ala Asp Tyr Gln Ala Ile Glu Thr Tyr Arg Arg  
 165 170 175

Ala Gln Pro Ile Ala Leu Ala Cys Ala Leu Asp Val Leu Leu Gly Glu  
 Page 49

180

09743PC.ST25.txt

185

190

His Asp Glu Glu Val Ser Ala Ala Glu Ala Gln Ala Trp Ser Asp Ala  
 195 200 205

Ser Arg Thr Pro Ala Arg Leu Arg Arg Phe Pro Gly Gly His Phe Tyr  
 210 215 220

Leu Ser Glu Gly Arg Asp Ala Val Ile Glu His Leu Leu Arg Arg Leu  
 225 230 235 240

Ala His Pro Asp Ala Leu Ser Arg Glu Val Ala  
 245 250

<210> 29  
 <211> 4317  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 29  
 atggatctgc ccccgattc ccgtaccgcc ctgcgcgact ggctgaccga gcagctcgcc 60  
 gacctgctcg gcgAACCGCT tgctgacgtg cgcgcctgg cggacgacga cgacctgctg 120  
 ggctgcggcc tcgactcgat ccgcctgatg tacctgcagg aacgcctgcg cgcgcgtggc 180  
 tcgacgctgg acttcgcca gttggcgca gccccctgcc tgggggcctg gctcgacctg 240  
 ctggcctgca gggaccggct gtccgcggcc gcaacggctg cgctgccgac ggccgaggat 300  
 cgcgatcagc cgttcgagct gtctccgtg cagcaggcct actggctggg acgtggcgcc 360  
 ggcgaggtgc tggcaacgt cagctgccat gccttctgg aattccgcac gcgggatgtc 420  
 gacccgcagc gcctggccgc ggcggcgag tgcgtgcgtc aacgccaccc gatgttgcgg 480  
 gcgcgcttcc tcgacggctcg ccagcagatc cttccgacgc cgccgctgtc ctgcttcgac 540  
 ctgcaggact ggcgcaccc acaggtggac gaggccgagc gcgactggca ggcgctgcgc 600  
 gactggcgcg cccatgaatg cctggcggtg gagcgcggcc aggtgttcct gctcgggctg 660  
 gtgcgcatgc cggcgccgca ggatcgccctc tggctgagtc tcgacctgtc tgccgcccgt 720  
 gtcgaaagcc tgcgcctgtc gctggccgaa ctgggcgttg cctacctggc gccggagcgc 780  
 ctggcgagc cgccggcgct gcatttcgccc gactacctgg cgacccgtgc ggcgcaacgc 840  
 gccgaggccg cggcgccggc ccgcgactac tggctggAAC gcctgcccgc cttgcccggac 900  
 gcccggccc tgccgttggc ctgcgcgccc gaaagcatcc gccagccgcg caccggcgc 960  
 ctggcattcc agcttccgc cggcgagagc cggcgccctgg agcgtctgtc cgccgacgtat 1020  
 ggcgtgacct tgtccagcgt gttcgctgc gccttcgcgc tggctctggc ggcgtggagc 1080  
 gaaagcgcgg aatttctcct caacgtgccg ttgttcgatc ggcattgccg cgcaccgcgt 1140  
 atcggcgagg tgatcgccga cttcaccacc ctgttgctgc tggagtgccg gatgcaggcc 1200

## 09743PC.ST25.txt

ggggtgtcct tcgcccaggc ggtgaagagc ttccagcgca acctccacgg agccatcgac	1260
cacgcccacat tccccgcctt ggaggtgctc cgcgaggcgc gccggcaggg ccagccacgc	1320
tcggcgcgg tggtgttcgc cagcaacctg ggcgaggagg gcttcgtccc ggccgccttc	1380
cgcgacgctt tcggcgatct ccacgacatg ctctcgacaga ccccgcaggt ctggctcgac	1440
caccagctct accgggtggg cgacggtatac ctgctggcct gggatagcgt cgtcggactg	1500
ttccccgaag gtctgccgga aaccatgttc gaagcctacg tggggctgct ccagcgtctc	1560
tgcgacagcg cctggggca gcccggcat ctggcggttc cctgggcgcga gcaggcgcgc	1620
cgggcctgc tcaacggcca gccggcatgc gccacggcgc gcaccctgca tcgcaacttc	1680
ttccttcgcg cggccgaggc gccggatgcc gacgcgtcgc tctatcgacga ccaacgtgtc	1740
acccgcggcg aactggccga gcgtgcgtcg cgcatcgccg gcggcctgcg cgaagccggg	1800
gtgcggcctg gcgacgcgtt cgaggtcagc ctggcgccgc gaccgcagca ggtcgcggcg	1860
gtattcggcg tgctcgccgc aggcgcctgc tacgtgccgc tggacatcga ccagccgccc	1920
gcacggcggc gcctgatcga agaggccgcc ggggtatgcc tggcgatcac cgaggaggac	1980
gatccgcagg cttgccgcc gcgcctggat gtccagcgcc tgctgcgcgg cccggcgctg	2040
gccgcggcccg tgccgctggc gccgcaggcg agtgcctatg tgcatacac ctcggcgtcc	2100
accggggtgtc ccaagggcgt cgaggtcagc cacgcggcgg cgatcaatac catcgacgcg	2160
ctgctcgacc tgctcggggt gaacgcacatcg gatgcgttgc tggcggtctc cgcgctggac	2220
ttcgatctgt cggcttcga cctgttcggc ggcctcgccg ccgggtgccag cctggcctcg	2280
ccggcccagg aacaggcgcg cgatgcgtcg gcctggcg aggctatcca gcggcatgcg	2340
gtgagcctgt ggaactcggc gccggccttg ctggagatgg ccctcagcct gccggcgagc	2400
caggccgact atcgcagtct gcgggcggtg ctgctgtccg gcgactgggt ggcctggac	2460
ctgccccggcc gcctgccc acgttgtgcc gaaggctgcc gcctgcattgt gctgggtggc	2520
gctaccgaag cgggcacatcg gtcgaacctg cagagcgtcg atacggtgcc gccgcactgg	2580
cgttcgattc cctacggccg gccattgccg ggacaggcct accgggtggt cgacacccac	2640
ggcgccgacg tgccggaccc ggtggtcggc gagctgtgga tcggcgccgc cagcctggcc	2700
cgcggctatc gcaacgcattcc cgaactcagc gcccggcggt tcgtccacga tgcccaggc	2760
cgcgttgcgcgcacatc gcacccggcga tcgcggtcgc tactggggcg acggtaaccct ggaattcctc	2820
ggtcgggtcg accagcaggt gaaagtgcgc ggccagcgcac tcgagttggg cgaggtggag	2880
gccgcgtgt gcccggcaggc tggcggtggag agcgccctgcg cggcggtgct cggcggtggc	2940
gtggcgagcc tcggcgccgg gctggtaccg cgcctggcgc cacggggcga aggctccatg	3000
gatctaccgg cgcacacagcc cttcgccggc ctggcagagg ccgaggcggt actcaccgg	3060
gaaatcctcg gcgcgctgct ggaggcgccg ctggagctag acgacggttt gcgcggcgc	3120

## 09743PC.ST25.txt

tggctggact ggctagcgga	ctccgcccgc	agcgcgctgc	cgtcgctcga	cgaggcgttg	3180
cgcggctcg gctggcaggc	cgcggggctg	accgcgatgg	gcaacgctct	gcgcggcctg	3240
ctcgccggcg aacaggcgcc	ggccgcgctg	ctcctcgatc	cctggctggc	gccgcaggcg	3300
gtggccgcgc gcctgcccga	cggccgcgag	gccctggcgc	gcctgctcga	agcgctgccc	3360
acgcccggctg cggcgaaacg	cctgcgggtg	gcgggtctgg	ataccgcgc	cgggctctgg	3420
ctcgaccagg gcatggcctc	gctgttgcgc	ccagggctgg	aactgaccct	cttcgaacgc	3480
agccgcgtcc tcctcgacgc	cgccgcacc	cgcttgcgg	aacggatcgt	ggtgcaggcg	3540
ctggacgacg gcctgctacc	tgccgagcac	ctcggtcgct	acgaccgggt	gatcagcttc	3600
gccgcgtgc acgcctacga	ggccagccgc	gaaggcctgg	cgctggcggc	ggcgctgctg	3660
cgcggcagg gccgcctgtt	gctggtggac	ctgctatgcg	agtcgccact	ggcgctgctc	3720
ggtgcggcct tgctcgacga	ccggccgctg	cgccctggcgg	agtcggcag	cctgttggcc	3780
gatctcgccg ctgcggact	ggcgccgcgt	tgccctgtggc	gcagcgagcg	gatcgccctg	3840
gtcgaggcgc tggcacccgg	actcgggctc	gacgcccgcg	cgctccaggc	cggcctggag	3900
caacgcctgc cccaggcgat	gcggcccgaa	cgcctgtgg	gcctgccaag	cctgcgcgtt	3960
aacggcaatg gcaagggtcga	tcgtcgccgc	ctggccgaga	gcatgaccgc	cgcactcgcc	4020
gagtgtcgtc acgagccctc	ggcggaggag	ccgctggaaag	ccatgagca	agcgctggcc	4080
gagtgtggg aagcggttct	caaacgccc	gtgcgtcg	gcgaggcgag	cttcttcagc	4140
ctcggccgcg acagcctgct	ggcgacccgc	ctgctggccg	gcatacgtga	gcgtttcgcc	4200
gtacgcctgg gcatggccga	cttctatcg	cagccgaccc	tggccggct	tgcccgccac	4260
ttgcaggtgc agaccgtcga	aatcgaggaa	acccaactgg	aagagggcgt	gctatga	4317

<210> 30  
 <211> 1438  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<400> 30

Met Asp Leu Pro Pro Asp Ser Arg Thr Ala Leu Arg Asp Trp Leu Thr  
 1 5 10 15

Glu Gln Leu Ala Asp Leu Leu Gly Glu Pro Leu Ala Asp Val Arg Ala  
 20 25 30

Leu Ala Asp Asp Asp Asp Leu Leu Gly Cys Gly Leu Asp Ser Ile Arg  
 35 40 45

Leu Met Tyr Leu Gln Glu Arg Leu Arg Ala Arg Gly Ser Thr Leu Asp  
 50 55 60

## 09743PC.ST25.txt

Phe Ala Gln Leu Ala Gln Arg Pro Cys Leu Gly Ala Trp Leu Asp Leu  
65 70 75 80

Leu Ala Cys Ala Asp Arg Leu Ser Ala Pro Ala Thr Val Ala Leu Pro  
85 90 95

Thr Ala Gln Asp Arg Asp Gln Pro Phe Glu Leu Ser Ser Val Gln Gln  
100 105 110

Ala Tyr Trp Leu Gly Arg Gly Ala Gly Glu Val Leu Gly Asn Val Ser  
115 120 125

Cys His Ala Phe Leu Glu Phe Arg Thr Arg Asp Val Asp Pro Gln Arg  
130 135 140

Leu Ala Ala Ala Ala Glu Cys Val Arg Gln Arg His Pro Met Leu Arg  
145 150 155 160

Ala Arg Phe Leu Asp Gly Arg Gln Gln Ile Leu Pro Thr Pro Pro Leu  
165 170 175

Ser Cys Phe Asp Leu Gln Asp Trp Arg Thr Leu Gln Val Asp Glu Ala  
180 185 190

Glu Arg Asp Trp Gln Ala Leu Arg Asp Trp Arg Ala His Glu Cys Leu  
195 200 205

Ala Val Glu Arg Gly Gln Val Phe Leu Leu Gly Leu Val Arg Met Pro  
210 215 220

Gly Gly Glu Asp Arg Leu Trp Leu Ser Leu Asp Leu Leu Ala Ala Asp  
225 230 235 240

Val Glu Ser Leu Arg Leu Leu Ala Glu Leu Gly Val Ala Tyr Leu  
245 250 255

Ala Pro Glu Arg Leu Ala Glu Pro Pro Ala Leu His Phe Ala Asp Tyr  
260 265 270

Leu Ala His Arg Ala Ala Gln Arg Ala Glu Ala Ala Ala Arg Ala Arg  
275 280 285

Asp Tyr Trp Leu Glu Arg Leu Pro Arg Leu Pro Asp Ala Pro Ala Leu  
290 295 300

Pro Leu Ala Cys Ala Pro Glu Ser Ile Arg Gln Pro Arg Thr Arg Arg  
305 310 315 320

## 09743PC.ST25.txt

Leu Ala Phe Gln Leu Ser Ala Gly Glu Ser Arg Arg Leu Glu Arg Leu  
325 330 335

Ala Ala Gln His Gly Val Thr Leu Ser Ser Val Phe Gly Cys Ala Phe  
340 345 350

Ala Leu Val Leu Ala Arg Trp Ser Glu Ser Ala Glu Phe Leu Leu Asn  
355 360 365

Val Pro Leu Phe Asp Arg His Ala Asp Asp Pro Arg Ile Gly Glu Val  
370 375 380

Ile Ala Asp Phe Thr Thr Leu Leu Leu Leu Glu Cys Arg Met Gln Ala  
385 390 395 400

Gly Val Ser Phe Ala Glu Ala Val Lys Ser Phe Gln Arg Asn Leu His  
405 410 415

Gly Ala Ile Asp His Ala Ala Phe Pro Ala Leu Glu Val Leu Arg Glu  
420 425 430

Ala Arg Arg Gln Gly Gln Pro Arg Ser Ala Pro Val Val Phe Ala Ser  
435 440 445

Asn Leu Gly Glu Glu Gly Phe Val Pro Ala Ala Phe Arg Asp Ala Phe  
450 455 460

Gly Asp Leu His Asp Met Leu Ser Gln Thr Pro Gln Val Trp Leu Asp  
465 470 475 480

His Gln Leu Tyr Arg Val Gly Asp Gly Ile Leu Leu Ala Trp Asp Ser  
485 490 495

Val Val Gly Leu Phe Pro Glu Gly Leu Pro Glu Thr Met Phe Glu Ala  
500 505 510

Tyr Val Gly Leu Leu Gln Arg Leu Cys Asp Ser Ala Trp Gly Gln Pro  
515 520 525

Ala Asp Leu Pro Leu Pro Trp Ala Gln Gln Ala Arg Arg Ala Leu Leu  
530 535 540

Asn Gly Gln Pro Ala Cys Ala Thr Ala Arg Thr Leu His Arg Asp Phe  
545 550 555 560

Phe Leu Arg Ala Ala Glu Ala Pro Asp Ala Asp Ala Leu Leu Tyr Arg  
565 570 575

## 09743PC.ST25.txt

Asp Gln Arg Val Thr Arg Gly Glu Leu Ala Glu Arg Ala Leu Arg Ile  
580 585 590

Ala Gly Gly Leu Arg Glu Ala Gly Val Arg Pro Gly Asp Ala Val Glu  
595 600 605

Val Ser Leu Pro Arg Gly Pro Gln Gln Val Ala Ala Val Phe Gly Val  
610 615 620

Leu Ala Ala Gly Ala Cys Tyr Val Pro Leu Asp Ile Asp Gln Pro Pro  
625 630 635 640

Ala Arg Arg Arg Leu Ile Glu Glu Ala Ala Gly Val Cys Leu Ala Ile  
645 650 655

Thr Glu Glu Asp Asp Pro Gln Ala Leu Pro Pro Arg Leu Asp Val Gln  
660 665 670

Arg Leu Leu Arg Gly Pro Ala Leu Ala Ala Pro Val Pro Leu Ala Pro  
675 680 685

Gln Ala Ser Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr Gly Val Pro  
690 695 700

Lys Gly Val Glu Val Ser His Ala Ala Ala Ile Asn Thr Ile Asp Ala  
705 710 715 720

Leu Leu Asp Leu Leu Arg Val Asn Ala Ser Asp Arg Leu Leu Ala Val  
725 730 735

Ser Ala Leu Asp Phe Asp Leu Ser Val Phe Asp Leu Phe Gly Gly Leu  
740 745 750

Gly Ala Gly Ala Ser Leu Val Leu Pro Ala Gln Glu Gln Ala Arg Asp  
755 760 765

Ala Ala Ala Trp Ala Glu Ala Ile Gln Arg His Ala Val Ser Leu Trp  
770 775 780

Asn Ser Ala Pro Ala Leu Leu Glu Met Ala Leu Ser Leu Pro Ala Ser  
785 790 795 800

Gln Ala Asp Tyr Arg Ser Leu Arg Ala Val Leu Leu Ser Gly Asp Trp  
805 810 815

Val Ala Leu Asp Leu Pro Gly Arg Leu Arg Pro Arg Cys Ala Glu Gly  
820 825 830

## 09743PC.ST25.txt

Cys Arg Leu His Val Leu Gly Gly Ala Thr Glu Ala Gly Ile Trp Ser  
835 840 845

Asn Leu Gln Ser Val Asp Thr Val Pro Pro His Trp Arg Ser Ile Pro  
850 855 860

Tyr Gly Arg Pro Leu Pro Gly Gln Ala Tyr Arg Val Val Asp Thr His  
865 870 875 880

Gly Arg Asp Val Pro Asp Leu Val Val Gly Glu Leu Trp Ile Gly Gly  
885 890 895

Ala Ser Leu Ala Arg Gly Tyr Arg Asn Asp Pro Glu Leu Ser Ala Arg  
900 905 910

Arg Phe Val His Asp Ala Gln Gly Arg Trp Tyr Arg Thr Gly Asp Arg  
915 920 925

Gly Arg Tyr Trp Gly Asp Gly Thr Leu Glu Phe Leu Gly Arg Val Asp  
930 935 940

Gln Gln Val Lys Val Arg Gly Gln Arg Ile Glu Leu Gly Glu Val Glu  
945 950 955 960

Ala Ala Leu Cys Ala Gln Ala Gly Val Glu Ser Ala Cys Ala Ala Val  
965 970 975

Leu Gly Gly Val Ala Ser Leu Gly Ala Val Leu Val Pro Arg Leu  
980 985 990

Ala Pro Arg Ala Glu Gly Ser Met Asp Leu Pro Ala Ala Gln Pro Phe  
995 1000 1005

Ala Gly Leu Ala Glu Ala Glu Ala Val Leu Thr Arg Glu Ile Leu  
1010 1015 1020

Gly Ala Leu Leu Glu Ala Pro Leu Glu Leu Asp Asp Gly Leu Arg  
1025 1030 1035

Arg Arg Trp Leu Asp Trp Leu Ala Asp Ser Ala Ala Ser Ala Leu  
1040 1045 1050

Pro Ser Leu Asp Glu Ala Leu Arg Arg Leu Gly Trp Gln Ala Ala  
1055 1060 1065

Gly Leu Thr Ala Met Gly Asn Ala Leu Arg Gly Leu Leu Ala Gly  
1070 1075 1080

## 09743PC.ST25.txt

Glu Gln Ala Pro Ala Ala Leu Leu Leu Asp Pro Trp Leu Ala Pro  
1085 1090 1095

Gln Ala Val Ala Ala Arg Leu Pro Asp Gly Arg Glu Ala Leu Ala  
1100 1105 1110

Arg Leu Leu Glu Ala Leu Pro Thr Pro Ala Ala Gly Glu Arg Leu  
1115 1120 1125

Arg Val Ala Val Leu Asp Thr Arg Ala Gly Leu Trp Leu Asp Gln  
1130 1135 1140

Gly Met Ala Ser Leu Leu Arg Pro Gly Leu Glu Leu Thr Leu Phe  
1145 1150 1155

Glu Arg Ser Arg Val Leu Leu Asp Ala Ala Ala Thr Arg Leu Pro  
1160 1165 1170

Glu Arg Ile Val Val Gln Ala Leu Asp Asp Gly Leu Leu Pro Ala  
1175 1180 1185

Glu His Leu Gly Arg Tyr Asp Arg Val Ile Ser Phe Ala Ala Leu  
1190 1195 1200

His Ala Tyr Glu Ala Ser Arg Glu Gly Leu Ala Leu Ala Ala Ala  
1205 1210 1215

Leu Leu Arg Pro Gln Gly Arg Leu Leu Leu Val Asp Leu Leu Cys  
1220 1225 1230

Glu Ser Pro Leu Ala Leu Leu Gly Ala Ala Leu Leu Asp Asp Arg  
1235 1240 1245

Pro Leu Arg Leu Ala Glu Leu Pro Ser Leu Leu Ala Asp Leu Ala  
1250 1255 1260

Ala Ala Gly Leu Ala Pro Arg Cys Leu Trp Arg Ser Glu Arg Ile  
1265 1270 1275

Ala Leu Val Glu Ala Leu Ala Pro Gly Leu Gly Leu Asp Ala Ala  
1280 1285 1290

Ala Leu Gln Ala Gly Leu Glu Gln Arg Leu Pro Gln Ala Met Arg  
1295 1300 1305

Pro Glu Arg Leu Trp Cys Leu Pro Ser Leu Pro Leu Asn Gly Asn  
1310 1315 1320

## 09743PC.ST25.txt

Gly Lys Val Asp Arg Arg Arg 1325 Leu Ala Glu Ser Met Thr Arg Ala 1330 1335

Leu Gly Glu Cys Arg His Glu 1340 Pro Ser Ala Glu Glu Pro Leu Glu 1345 1350

Ala His Glu Gln Ala Leu Ala 1355 Glu Cys Trp Glu Ala Val Leu Lys 1360 1365

Arg Pro Val Arg Arg Arg Glu 1370 Ala Ser Phe Phe Ser Leu Gly Gly 1375 1380

Asp Ser Leu Leu Ala Thr Arg 1385 Leu Leu Ala Gly Ile Arg Glu Arg 1390 1395

Phe Gly Val Arg Leu Gly Met 1400 Ala Asp Phe Tyr Arg Gln Pro Thr 1405 1410

Leu Ala Gly Leu Ala Arg His 1415 Leu Gln Val Gln Thr Val Glu Ile 1420 1425

Glu Glu Thr Gln Leu Glu Glu 1430 Gly Val Leu 1435

<210> 31  
<211> 5430  
<212> DNA  
<213> Pseudomonas aeruginosa

<400> 31	
atgagcctcg gcaaactgct ggaaacctgc cgcagccggc gcatcgaact ctggagcgag	60
gcggggccgccc tgcgctatcg cgcgcgcgcag ggtgcgcctcg acgcgcgcct cgccgcgcgc	120
ctgcggggcccg agcgcgcggc cctgctggaa cacctggaa acgcgcgcgcgcgcgcgcgc	180
gaacccgaca tggcccacca gcgcgtcccg ctgaccccg tgcaggccgc ctacgtgctg	240
ggccgcgcagg cggccttcga ctacggcggt aacgcctgac agctgtacgc cgagtacgac	300
tggccggcccg acaccgatcc ggccgcgcctg gaggcgccct ggaacgcgcgc ggtcgagcgc	360
cacccgatgc tgcgcgcggt gatcgaggac aacgcctggc agcgcgtgct gcccgcgggt	420
ccctggcagc ggctgaccgt gcatgcctgc gcggggctcg acgaggccgc tttccaggcg	480
cacctggagc gggtccgcga acgcctcgac cacgcctgcg cggcgctcga ccagtggccg	540
gtcctgcgcgc ccgagctgag tatcgccgg gatgcctgcg tactgcactg ctcgggtggat	600
ttcacccctgg tcgactacgc cagcctgcaa ttgctgcttgc gcaatggcg ccgcgcgtat	660
ctcgatccgc aatggacggc ggaaccgctg gaggcgaccc tccgcgacta tgcggcgtc	720
gagcagcgcc gacgcccagtc gccagcctgg cagcgcgacc gcgactggtg gctggcgctg	780

## 09743PC.ST25.txt

ctcgacgcgc taccggggcg tcccgacctg ccgctgcggg tgcagccgga caccgggtcc	840
acgcgcttcc ggcacttcca cgcgcgcctc gacgaggccg cctggcaggc gctcgccg	900
cgcgcggcg aacacggcct gagcgctgcc ggcgtggcct tggccgcctt cgccgagacc	960
atcggtcgct ggagccaggc accggcggtc tgtctcaacc tgacggtact caaccggccg	1020
ccgctgcattc cgcagctggc gcaggtgctc ggtgacttca ccgcgcctcag cctgctggca	1080
gtggacagcc gccacggcga cagttcgtc gagcgtgccc gacgcattcg cgagcagatg	1140
ttcgacgacc tcgaccaccc gaccttcagc ggcgtcgacc tgctgcgcga actggcgcc	1200
cggcgtggtc gcggcgccga tctgatgccc gtgggtttca ccagtggcat cggcagcgtg	1260
cagcgcctgc tcggcgatgg cgaggcgccg cgcgccacac gctacatgtat cagccagacc	1320
ccgcaggtct ggctggactg ccaggtcacc gaccagttcg gcggcctgga gatcggctgg	1380
gacgtacgcc tcgggttgg ccccgagggc caggcggaaag ccatgttcga cgacttcgtc	1440
gggctgctcc gcgcctggc gcagagcccg cgccctgga ccgacggcga tgccacggaa	1500
cccgtcgagg cgccgcccga ggcgttgcgc ggtagtgcgc ggagcatcgc cgccggtttc	1560
gccgagcgtg ccctgctgac ccccgacgcc acggcgatcc acgatgcgcg cggcagctac	1620
agctaccgcc aggtcgccca gcacgccagc gcccgcgcg gcgtcctgga agcgcacggc	1680
gcggggccgtg gccggcggtt cgcggtgatg ctgcccggaa gcccgcgcgca attggtcgcg	1740
gtgatcgca tcctccaggc cggcgccgc tatgtgcgg tggacatccg ccagcctccg	1800
ctgcggcgcc aggcgatcct cgccagcgcc gaagtggtcg cgctggctcg cctggaaagc	1860
gatgtcccg acgtcggtcg cgccctgcgtg gccatcgacc ggctggccgc cgacagcgcc	1920
tggccgcac cgcccgccggc ggaggtggcg gcggacgacc tcgcctacgt gatctacacc	1980
tccggctcca cccgcacgcc aaaggcggtg atgctcagcc atgcggcggt gagcaacacg	2040
ctgctcgaca tcaaccagcg ctacggcgtc gacgcacacg accgcgtcct cggcctcgcc	2100
gagctgagct tcgacacctc ggtctacgac ttcttcggcg ccaccgcggc gggggcccg	2160
gtggtcctcc cggaccggc gcgcggcagc gatccatcgc actggcgga actgctggaa	2220
cgccacgcca tcacccctgtg gaactcggtg ccggcccaag gccagatgct catcgattac	2280
ctggagagcg agccgcaacg tcacccgtcg ggaccgcgt gcgtgctcg gtccggtgac	2340
tggattccgg tcagcctgcc gacccgctgg tggcgccgtt ggccggacag cgcgctgttc	2400
agcctggcg gcgcaccga ggcggcgatc tggtcgtatcg agcagccgtat ccgccccgag	2460
cacaccgagc tggccagcat cccttatggc cgtccctgc gcggcgagag cgtgaaagtc	2520
ctggatgccc gcgggcggcg ctgcccgcgc ggctgcgcg gcgagatcca tatcgccgg	2580
gtgggcctgg cgctcggtca cgccggcgat ccgcagcgca ccgcgaacg ctgcgtccgt	2640
caccccgatg gccgtcgccct gtatcgacc gcgcacctcg ggcgttaccc ggccgacggc	2700

## 09743PC.ST25.txt

agcatcgagt	tcctcgcccg	cgaggacgac	caggtgaaga	ttcgcggcca	ccgcacatcgaa	2760
ctggccgaac	tggacgcccgc	gctgtgcgt	catccgcagg	tcaacctggc	ggccaccgtg	2820
gtgctcgccg	agacccacga	gcgcagcctg	gccagctcg	tcaccctgca	tgcgcgggtg	2880
gaggctggcg	aggatcccg	tacggcgctc	gacgcggtgc	gccagcgggc	ggcccaggcc	2940
ttgcgcgcg	actggggcag	cgaggaggc	atcgccgcgg	cggtggccgc	actcgaccgt	3000
gcctgcctcg	cctcggttggc	cgcctggctg	gccggcagcg	gtctgttcgc	cagtgcgacg	3060
ccgctggact	tagccacacct	gtgcacagcgc	ctgggtatcg	ccgaggcgcg	ccagcgcctg	3120
ctgcgccact	gttgcgcaca	actggaggag	ggcggctacc	tgcgcgcgcga	gggcgagggc	3180
tggctgggct	gcgcgcgagcg	tcccgcgcag	agtccggagg	acgcctggac	ggcgttcgcc	3240
ggctgcgcgc	cggcggcgct	ctggccggcc	gagctggctg	cctacctgca	tgacagcgcg	3300
caatccctcg	gcgagcaact	ggccgggcgg	atcagcccg	ccgcgcgtat	gttcccgag	3360
ggctcggcgc	gcatcgccga	ggccatgtac	agccagggcc	tgcatgcaca	ggcgctgcac	3420
gaggccatgg	ccgaggccat	cgcgcgcata	gtcgagcgc	agccgcaacg	gcgcgtggcg	3480
ctgctggagc	ttggcgccgg	caccgcgc	gccagccga	cggtgatcg	ccgggttggcg	3540
ccgctgggtc	agcgaggggc	ggaggtggac	tacctgtca	ccgacgtttc	cagctacttc	3600
ctcgccgcgc	ccgcgcagcg	cttcgcgcac	cagccgtgg	tacgcttcgg	ccgcttcgac	3660
atgaacggcg	atcttctcg	ccagggcg	gcccgcact	cggtggat	cctgctcagc	3720
tccggggcct	tgaacaacgc	gctggacacc	ccggcgctgc	tggccggcct	gcgcgagttg	3780
ctgagcgcgc	acgcctggct	ggtgatccag	gaactgacgc	gcgagcacaa	cgagatcagc	3840
gtcagccaga	gcctgtatgt	ggaaaacccg	cgcgacctcc	gcgacgagcg	ccgccaactg	3900
ttcgtccaca	ccgggcaatg	gctggagtgg	ctggcggcac	agggtggcga	cctggattgt	3960
ggggtgttgc	cgcggggcag	cgctctcgac	ctgcttgct	acgatgtcct	gctggctcgc	4020
tgcaagaccg	accgcgcggc	cctggagccg	gccgagctgc	tggccttcgt	cgaagcgcgg	4080
gtgccgcgc	acatgctccc	ggcgacgttg	cgcgtgc	aacgcctgca	ggtcacccgc	4140
aacggcaaga	tcgaccgcaa	ggccctgacc	ggcttgc	gccagcccc	ggcggacatt	4200
cggcatggcg	tcgcgcaggc	accggccgac	gaactggaga	atgcgctgct	ggcactctgg	4260
cgggaggtgc	tggacaaccc	gtcgctggc	gtcgagcaag	acttcttcgg	ggccggcg	4320
gactcgctgt	tgatcgccca	gttgatcgcc	cgtttgcgcg	aacgactgg	aagcgcccg	4380
cggcatccgt	tcgatcgcc	gctacgctgg	gctcgatcg	agccgacgac	gcgcggcctg	4440
gccgaacgccc	tgcgacgcgc	gccggaagag	ggccgtggc	cagccctggc	cgcggcgcgc	4500
ggcgatcgccc	cggcgccggc	cggcatgtcg	cgcgcacccgc	tgcgcgagg	cgcgggtggcg	4560
ctcgaccgc	tggtgcgcct	ggtgcgcggc	gagggcg	cgccgggtgc	ggtccacgaa	4620

## 09743PC.ST25.txt

ggcctcggca	cgctactgcc	gtaccgccc	ctgcttcgcg	ccctgggtga	ggggcggccg	4680
ttgctgggc	tggccgtgca	tgacagcgac	gcctacctgg	cgatccccgc	cgagcatctc	4740
aacgcctgcc	tcggccgccc	ctacgcccag	gcgctccatc	gcgcgggct	acgcgaggtc	4800
gacctgctcg	gctactgctc	cggcgggctg	gtcgccctgg	agaccgccaa	gtccctggtc	4860
cagcgcgggg	tgcgcgtgca	ccaaactggat	atcgctcca	gctaccggat	tccctaccgg	4920
gtggacgacg	agcgccctgct	gttggtcagc	ttcgccgcga	ccctcggcct	ggataccgcg	4980
gcgctcggct	tcccccgcgc	ggaacgtctc	ggccaggcgg	tgcaggcggc	gctcgccag	5040
acaccggagc	gcctggtcgc	cgagggcgctg	gcggggctgc	cgggcctggc	cgatctcgct	5100
gcccctgcgc	gccgcgtgct	acagggcgcc	agcggtagcg	ccgacgccgt	cagcgtcga	5160
cgcgacaccc	tctaccggct	gttctgtcac	tcgggtgcgtg	ccagccaggc	cgaggcgcgg	5220
gagccctacg	tcggcgcgct	gcggctgttc	gtgccggacg	ccggcaaccc	attggtgccg	5280
cgctacgccc	aggctctgga	gacccaatgg	cggccgcggc	cgcttggcgc	gtgcggcatc	5340
cacgaggtgc	cggcgggca	cttcgactgc	ctggcgaag	ccctggcgc	atccttgc	5400
aaaccatgc	cagaggaggc	gagccgatga				5430

&lt;210&gt; 32

&lt;211&gt; 1809

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas aeruginosa

&lt;400&gt; 32

Met	Ser	Leu	Gly	Glu	Leu	Leu	Glu	Thr	Cys	Arg	Ser	Arg	Arg	Ile	Glu
1					5			10						15	

Leu	Trp	Ser	Glu	Ala	Gly	Arg	Leu	Arg	Tyr	Arg	Ala	Pro	Gln	Gly	Ala
				20				25					30		

Leu	Asp	Ala	Gly	Leu	Ala	Glu	Arg	Leu	Arg	Ala	Glu	Arg	Glu	Ala	Leu
				35		40					45				

Leu	Glu	His	Leu	Glu	Gly	Gly	Pro	Gly	Trp	Arg	Ala	Glu	Pro	Asp	Met
				50		55			60						

Ala	His	Gln	Arg	Phe	Pro	Leu	Thr	Pro	Val	Gln	Ala	Ala	Tyr	Val	Leu
				65		70			75				80		

Gly	Arg	Gln	Ala	Ala	Phe	Asp	Tyr	Gly	Gly	Asn	Ala	Cys	Gln	Leu	Tyr
				85				90					95		

Ala	Glu	Tyr	Asp	Trp	Pro	Ala	Asp	Thr	Asp	Pro	Ala	Arg	Leu	Glu	Ala
				100				105					110		

## 09743PC.ST25.txt

Ala Trp Asn Ala Met Val Glu Arg His Pro Met Leu Arg Ala Val Ile  
115 120 125

Glu Asp Asn Ala Trp Gln Arg Val Leu Pro Glu Val Pro Trp Gln Arg  
130 135 140

Leu Thr Val His Ala Cys Ala Gly Leu Asp Glu Ala Ala Phe Gln Ala  
145 150 155 160

His Leu Glu Arg Val Arg Glu Arg Leu Asp His Ala Cys Ala Ala Leu  
165 170 175

Asp Gln Trp Pro Val Leu Arg Pro Glu Leu Ser Ile Gly Arg Asp Ala  
180 185 190

Cys Val Leu His Cys Ser Val Asp Phe Thr Leu Val Asp Tyr Ala Ser  
195 200 205

Leu Gln Leu Leu Leu Gly Glu Trp Arg Arg Arg Tyr Leu Asp Pro Gln  
210 215 220

Trp Thr Ala Glu Pro Leu Glu Ala Thr Phe Arg Asp Tyr Val Gly Val  
225 230 235 240

Glu Gln Arg Arg Arg Gln Ser Pro Ala Trp Gln Arg Asp Arg Asp Trp  
245 250 255

Trp Leu Ala Arg Leu Asp Ala Leu Pro Gly Arg Pro Asp Leu Pro Leu  
260 265 270

Arg Val Gln Pro Asp Thr Arg Ser Thr Arg Phe Arg His Phe His Ala  
275 280 285

Arg Leu Asp Glu Ala Ala Trp Gln Ala Leu Gly Ala Arg Ala Gly Glu  
290 295 300

His Gly Leu Ser Ala Ala Gly Val Ala Leu Ala Ala Phe Ala Glu Thr  
305 310 315 320

Ile Gly Arg Trp Ser Gln Ala Pro Ala Phe Cys Leu Asn Leu Thr Val  
325 330 335

Leu Asn Arg Pro Pro Leu His Pro Gln Leu Ala Gln Val Leu Gly Asp  
340 345 350

Phe Thr Ala Leu Ser Leu Leu Ala Val Asp Ser Arg His Gly Asp Ser  
355 360 365

## 09743PC.ST25.txt

Phe Val Glu Arg Ala Arg Arg Ile Gly Glu Gln Met Phe Asp Asp Leu  
370 375 380

Asp His Pro Thr Phe Ser Gly Val Asp Leu Leu Arg Glu Leu Ala Arg  
385 390 395 400

Arg Arg Gly Arg Gly Ala Asp Leu Met Pro Val Val Phe Thr Ser Gly  
405 410 415

Ile Gly Ser Val Gln Arg Leu Leu Gly Asp Gly Glu Ala Pro Arg Ala  
420 425 430

Pro Arg Tyr Met Ile Ser Gln Thr Pro Gln Val Trp Leu Asp Cys Gln  
435 440 445

Val Thr Asp Gln Phe Gly Gly Leu Glu Ile Gly Trp Asp Val Arg Leu  
450 455 460

Gly Leu Phe Pro Glu Gly Gln Ala Glu Ala Met Phe Asp Asp Phe Val  
465 470 475 480

Gly Leu Leu Arg Arg Leu Ala Gln Ser Pro Arg Ala Trp Thr Asp Gly  
485 490 495

Asp Ala Thr Glu Pro Val Glu Ala Pro Pro Gln Ala Leu Pro Gly Ser  
500 505 510

Ala Arg Ser Ile Ala Ala Gly Phe Ala Glu Arg Ala Leu Leu Thr Pro  
515 520 525

Asp Ala Thr Ala Ile His Asp Ala Ala Gly Ser Tyr Ser Tyr Arg Gln  
530 535 540

Val Ala Gln His Ala Ser Ala Leu Arg Arg Val Leu Glu Ala His Gly  
545 550 555 560

Ala Gly Arg Gly Arg Arg Val Ala Val Met Leu Pro Lys Ser Ala Ala  
565 570 575

Gln Leu Val Ala Val Ile Gly Ile Leu Gln Ala Gly Ala Ala Tyr Val  
580 585 590

Pro Val Asp Ile Arg Gln Pro Pro Leu Arg Arg Gln Ala Ile Leu Ala  
595 600 605

Ser Ala Glu Val Val Ala Leu Val Cys Leu Glu Ser Asp Val Pro Asp  
610 615 620

## 09743PC.ST25.txt

Val Gly Cys Ala Cys Val Ala Ile Asp Arg Leu Ala Ala Asp Ser Ala  
625 630 635 640

Trp Pro Pro Pro Ala Ala Glu Val Ala Ala Asp Asp Leu Ala Tyr  
645 650 655

Val Ile Tyr Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Val Met Leu  
660 665 670

Ser His Ala Ala Val Ser Asn Thr Leu Leu Asp Ile Asn Gln Arg Tyr  
675 680 685

Gly Val Asp Ala Asn Asp Arg Val Leu Gly Leu Ala Glu Leu Ser Phe  
690 695 700

Asp Leu Ser Val Tyr Asp Phe Phe Gly Ala Thr Ala Ala Gly Ala Gln  
705 710 715 720

Val Val Leu Pro Asp Pro Ala Arg Gly Ser Asp Pro Ser His Trp Ala  
725 730 735

Glu Leu Leu Glu Arg His Ala Ile Thr Leu Trp Asn Ser Val Pro Ala  
740 745 750

Gln Gly Gln Met Leu Ile Asp Tyr Leu Glu Ser Glu Pro Gln Arg His  
755 760 765

Leu Pro Gly Pro Arg Cys Val Leu Trp Ser Gly Asp Trp Ile Pro Val  
770 775 780

Ser Leu Pro Thr Arg Trp Trp Arg Arg Trp Pro Asp Ser Ala Leu Phe  
785 790 795 800

Ser Leu Gly Gly Ala Thr Glu Ala Ala Ile Trp Ser Ile Glu Gln Pro  
805 810 815

Ile Arg Pro Gln His Thr Glu Leu Ala Ser Ile Pro Tyr Gly Arg Ala  
820 825 830

Leu Arg Gly Gln Ser Val Glu Val Leu Asp Ala Arg Gly Arg Arg Cys  
835 840 845

Pro Pro Gly Val Arg Gly Glu Ile His Ile Gly Gly Val Gly Leu Ala  
850 855 860

Leu Gly Tyr Ala Gly Asp Pro Gln Arg Thr Ala Glu Arg Phe Val Arg  
865 870 875 880

## 09743PC.ST25.txt

His Pro Asp Gly Arg Arg Leu Tyr Arg Thr Gly Asp Leu Gly Arg Tyr  
885 890 895

Leu Ala Asp Gly Ser Ile Glu Phe Leu Gly Arg Glu Asp Asp Gln Val  
900 905 910

Lys Ile Arg Gly His Arg Ile Glu Leu Ala Glu Leu Asp Ala Ala Leu  
915 920 925

Cys Ala His Pro Gln Val Asn Leu Ala Ala Thr Val Val Leu Gly Glu  
930 935 940

Thr His Glu Arg Ser Leu Ala Ser Phe Val Thr Leu His Ala Pro Val  
945 950 955 960

Glu Ala Gly Glu Asp Pro Arg Thr Ala Leu Asp Ala Val Arg Gln Arg  
965 970 975

Ala Ala Gln Ala Leu Arg Arg Asp Trp Gly Ser Glu Glu Gly Ile Ala  
980 985 990

Ala Ala Val Ala Ala Leu Asp Arg Ala Cys Leu Ala Ser Leu Ala Ala  
995 1000 1005

Trp Leu Ala Gly Ser Gly Leu Phe Ala Ser Ala Thr Pro Leu Asp  
1010 1015 1020

Leu Ala Thr Leu Cys Gln Arg Leu Gly Ile Ala Glu Ala Arg Gln  
1025 1030 1035

Arg Leu Leu Arg His Trp Leu Arg Gln Leu Glu Glu Gly Gly Tyr  
1040 1045 1050

Leu Arg Ala Glu Gly Glu Gly Trp Leu Gly Cys Ala Glu Arg Pro  
1055 1060 1065

Ala Gln Ser Pro Glu Asp Ala Trp Thr Ala Phe Ala Gly Cys Ala  
1070 1075 1080

Pro Ala Ala Leu Trp Pro Ala Glu Leu Val Ala Tyr Leu Arg Asp  
1085 1090 1095

Ser Ala Gln Ser Leu Gly Glu Gln Leu Ala Gly Arg Ile Ser Pro  
1100 1105 1110

Ala Ala Leu Met Phe Pro Gln Gly Ser Ala Arg Ile Ala Glu Ala  
1115 1120 1125

## 09743PC.ST25.txt

Met Tyr Ser Gln Gly Leu His Ala Gln Ala Leu His Glu Ala Met  
1130 1135 1140

Ala Glu Ala Ile Ala Ala Ile Val Glu Arg Gln Pro Gln Arg Arg  
1145 1150 1155

Trp Arg Leu Leu Glu Leu Gly Ala Gly Thr Ala Ala Ala Ser Arg  
1160 1165 1170

Thr Val Ile Ala Arg Leu Ala Pro Leu Val Gln Arg Gly Ala Glu  
1175 1180 1185

Val Asp Tyr Leu Phe Thr Asp Val Ser Ser Tyr Phe Leu Ala Ala  
1190 1195 1200

Ala Arg Glu Arg Phe Ala Asp Gln Pro Trp Val Arg Phe Gly Arg  
1205 1210 1215

Phe Asp Met Asn Gly Asp Leu Leu Asp Gln Gly Val Ala Pro His  
1220 1225 1230

Ser Val Asp Ile Leu Leu Ser Ser Gly Ala Leu Asn Asn Ala Leu  
1235 1240 1245

Asp Thr Pro Ala Leu Leu Ala Gly Leu Arg Glu Leu Leu Ser Ala  
1250 1255 1260

Asp Ala Trp Leu Val Ile Gln Glu Leu Thr Arg Glu His Asn Glu  
1265 1270 1275

Ile Ser Val Ser Gln Ser Leu Met Met Glu Asn Pro Arg Asp Leu  
1280 1285 1290

Arg Asp Glu Arg Arg Gln Leu Phe Val His Thr Gly Gln Trp Leu  
1295 1300 1305

Glu Trp Leu Ala Ala Gln Gly Gly Asp Leu Ala Cys Gly Val Val  
1310 1315 1320

Pro Pro Gly Ser Ala Leu Asp Leu Leu Gly Tyr Asp Val Leu Leu  
1325 1330 1335

Ala Arg Cys Lys Thr Asp Arg Ala Arg Leu Glu Pro Ala Glu Leu  
1340 1345 1350

Leu Ala Phe Val Glu Ala Arg Val Pro Arg Tyr Met Leu Pro Ala  
1355 1360 1365

## 09743PC.ST25.txt

Gln Leu Arg Val Leu Glu Arg Leu Pro Val Thr Gly Asn Gly Lys  
1370 1375 1380

Ile Asp Arg Lys Ala Leu Thr Gly Phe Ala Arg Gln Pro Gln Ala  
1385 1390 1395

Asp Leu Arg His Gly Val Ala Gln Ala Pro Ala Asp Glu Leu Glu  
1400 1405 1410

Asn Ala Leu Leu Ala Leu Trp Arg Glu Val Leu Asp Asn Pro Ser  
1415 1420 1425

Leu Gly Val Glu Gln Asp Phe Phe Gly Ala Gly Gly Asp Ser Leu  
1430 1435 1440

Leu Ile Ala Gln Leu Ile Ala Arg Leu Arg Glu Arg Leu Glu Ser  
1445 1450 1455

Ala Arg Arg His Pro Phe Asp Arg Leu Leu Arg Trp Ala Leu Ser  
1460 1465 1470

Gln Pro Thr Pro Arg Gly Leu Ala Glu Arg Leu Arg Ser Ala Pro  
1475 1480 1485

Glu Glu Gly Arg Gly Pro Ala Leu Ala Ala Ala Arg Gly Val Ala  
1490 1495 1500

Pro Ala Pro Ala Gly Met Ser Arg Ala Pro Leu Ala Glu Gly Ala  
1505 1510 1515

Val Ala Leu Asp Pro Leu Val Arg Leu Val Pro Gly Glu Gly Val  
1520 1525 1530

Pro Arg Val Leu Val His Glu Gly Leu Gly Thr Leu Leu Pro Tyr  
1535 1540 1545

Arg Pro Leu Leu Arg Ala Leu Gly Glu Gly Arg Pro Leu Leu Gly  
1550 1555 1560

Leu Ala Val His Asp Ser Asp Ala Tyr Leu Ala Ile Pro Ala Glu  
1565 1570 1575

His Leu Asn Ala Cys Leu Gly Arg Arg Tyr Ala Glu Ala Leu His  
1580 1585 1590

Arg Ala Gly Leu Arg Glu Val Asp Leu Leu Gly Tyr Cys Ser Gly  
1595 1600 1605

## 09743PC.ST25.txt

Gly Leu Val Ala Leu Glu Thr Ala Lys Ser Leu Val Gln Arg Gly  
 1610 1615 1620

Val Arg Val Arg Gln Leu Asp Ile Val Ser Ser Tyr Arg Ile Pro  
 1625 1630 1635

Tyr Arg Val Asp Asp Glu Arg Leu Leu Leu Phe Ser Phe Ala Ala  
 1640 1645 1650

Thr Leu Gly Leu Asp Thr Ala Ala Leu Gly Phe Pro Ala Pro Glu  
 1655 1660 1665

Arg Leu Gly Gln Ala Val Gln Ala Ala Leu Ala Gln Thr Pro Glu  
 1670 1675 1680

Arg Leu Val Ala Glu Ala Leu Ala Gly Leu Pro Gly Leu Ala Asp  
 1685 1690 1695

Leu Val Ala Leu Arg Gly Arg Val Leu Gln Ala Ala Ser Gly Ser  
 1700 1705 1710

Ala Asp Ala Val Ser Val Glu Arg Asp Thr Leu Tyr Arg Leu Phe  
 1715 1720 1725

Cys His Ser Val Arg Ala Ser Gln Ala Glu Ala Pro Glu Pro Tyr  
 1730 1735 1740

Val Gly Ala Leu Arg Leu Phe Val Pro Asp Ala Gly Asn Pro Leu  
 1745 1750 1755

Val Pro Arg Tyr Ala Glu Ala Leu Glu Thr Gln Trp Arg Ala Ala  
 1760 1765 1770

Ala Leu Gly Ala Cys Gly Ile His Glu Val Pro Gly Gly His Phe  
 1775 1780 1785

Asp Cys Leu Gly Glu Ala Leu Ala Gln Ser Leu Ser Lys Pro Met  
 1790 1795 1800

Pro Glu Glu Ala Ser Arg  
 1805

<210> 33  
 <211> 1713  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 33  
 gtgaccgg tgctgtggcg cctgctgcgc acctatcgct ggcggctggc ggcggccatg  
 Page 68

## 09743PC.ST25.txt

gggttgcagg ccctggccgg gctctgctcg ctgttgcctt gcatgccttct cgcctggctc 120  
 gccgagccgc tggcgccgg ccaggcgccag ccggccctgc tggccctggt gctgctggcg 180  
 gtgctggcct ggctggcctg ccaggcgctg gccgcgcacc tggcccaccc ggtcgacgcg 240  
 gacctctgca acgacactgca cctgcgcctg ctggcgccacc tgcaacggct gccgctggac 300  
 tggttcggtc gccagggccc ggacggcgctg ggcgcgcctcg tggagcagga cgtgcgggccc 360  
 ctgcaccaac tgatcgccca cgctcccaac gatctcagca acctgttggt ggtgcgcctc 420  
 gtcgcgttgc tctggctggc ctggctgcac ccctggctgc tgctgttctg cctgctgccc 480  
 ctgggtctgg ccgcgcggcc cttcctgctg ctgcgcctgg cgcgctaccg cgacctggtg 540  
 ctgcggcgca acgcccgcgt ggaaaggctc tggcgact atggcgaatt cgcccacaac 600  
 ctgctgctgg cccgacagta ccccgccgc ggcataacaac agggcgccga ggcgtcggcg 660  
 gcggccctcg gcgaagcggtt cggcgctgg gtgaagcggg tggccaccc cgccgcgtg 720  
 gtctacgtgc agttgtcgac gccctggctg ctggcctggg tcctgctcgg cgcgctggcc 780  
 ctggatgccc tcggcggtgcc gctggcgctc ggccaggcct gtgccttcct gtcctgctg 840  
 cgggccttgg ctgccccggt gcaggcgctc ggccacggcg ggcacgcgt gctggcgcg 900  
 cgccgcgcgg ctagcgcct gcagcagggtt ttcgaccagg cgccgctggc cgagggccgc 960  
 tcgaccgcg agccggtcga tggcgccgtg ggcgtgcacg gcctggcca tgcctatgaa 1020  
 ggcgtggagg tcctggccga tatcgatctg gagctggagg atggcagcct ggtggccctg 1080  
 gtcggtccct cgggcgtccgg caagagcacc ctgctgcacc tgctggcgcg ctacatggac 1140  
 ggcgcgcgcg gcaactgga gttggcgcc ctggactga aggacatgcc tgatgcgtg 1200  
 cgccatcgcc atatcgccgt ggtcgccag caggcgccgg cgctggagat atccctggcc 1260  
 gacaacattt ccctgttccg ccccgatgcc gatctccagg agattcgcca ggccgcgcgt 1320  
 gacgcctgcc tcgacgagcg catcatggcc ctgcccgtg gctacgacag cgtgcgggga 1380  
 cgccgacctgc aactgtccgg cggcgaaactg caacgactgg ccctggcccg tgcgctgcta 1440  
 tcgcccggcga gcctgttgct gtcgacgag ccaacctcgg cgctggatcc gcagaccgcc 1500  
 cggcagggtcc tgcgcaaccc ggcgaaacgc ggcgggtggcc ggacccgggt gatcgctgcc 1560  
 catcgctctgg ccgaagtcaag cgatcgccgac ctgatccctgg tgctggtcgc tggccgtctg 1620  
 gtcgaacgcg gcgagcacgc ggcgctgttg gcccggacg ggcctatgc gcgcttgc 1680  
 cgtgaacaga acggcgccga ggtggccggca tga 1713

<210> 34  
 <211> 570  
 <212> PRT  
 <213> Pseudomonas aeruginosa  
 <400> 34

## 09743PC.ST25.txt

Met Thr Pro Val Leu Trp Arg Leu Leu Arg Thr Tyr Arg Trp Arg Leu  
1 5 10 15

Ala Ala Ala Met Gly Leu Gln Ala Leu Ala Gly Leu Cys Ser Leu Leu  
20 25 30

Pro Trp Met Leu Leu Ala Trp Leu Ala Glu Pro Leu Ala Arg Gly Gln  
35 40 45

Ala Gln Pro Ala Leu Leu Ala Leu Val Leu Leu Ala Val Leu Ala Trp  
50 55 60

Leu Gly Cys Gln Ala Leu Ala Ala His Leu Ala His Arg Val Asp Ala  
65 70 75 80

Asp Leu Cys Asn Asp Leu Arg Leu Arg Leu Leu Ala His Leu Gln Arg  
85 90 95

Leu Pro Leu Asp Trp Phe Gly Arg Gln Gly Pro Asp Gly Val Ala Arg  
100 105 110

Leu Val Glu Gln Asp Val Arg Ala Leu His Gln Leu Ile Ala His Ala  
115 120 125

Pro Asn Asp Leu Ser Asn Leu Leu Val Val Pro Leu Val Ala Leu Leu  
130 135 140

Trp Leu Ala Trp Leu His Pro Trp Leu Leu Leu Phe Cys Leu Leu Pro  
145 150 155 160

Leu Val Leu Ala Ala Ala Gly Phe Leu Leu Leu Arg Ser Ala Arg Tyr  
165 170 175

Arg Asp Leu Val Leu Arg Arg Asn Ala Ala Leu Glu Arg Leu Ser Ala  
180 185 190

Asp Tyr Gly Glu Phe Ala His Asn Leu Leu Leu Ala Arg Gln Tyr Pro  
195 200 205

Gly Ala Gly Ile Gln Gln Gly Ala Glu Ala Ser Ala Ala Ala Phe Gly  
210 215 220

Glu Ala Phe Gly Ala Trp Val Lys Arg Val Gly His Leu Ala Ala Leu  
225 230 235 240

Val Tyr Val Gln Leu Ser Thr Pro Trp Leu Leu Ala Trp Val Leu Leu  
245 250 255

09743PC.ST25.txt

Gly Ala Leu Ala Leu Asp Ala Leu Gly Val Pro Leu Ala Leu Gly Gln  
260 265 270

Ala Cys Ala Phe Leu Leu Leu Leu Arg Ala Leu Ala Ala Pro Val Gln  
275 280 285

Ala Leu Gly His Gly Gly Asp Ala Leu Leu Gly Ala Arg Ala Ala Ala  
290 295 300

Glu Arg Leu Gln Gln Val Phe Asp Gln Ala Pro Leu Ala Glu Gly Arg  
305 310 315 320

Ser Thr Arg Glu Pro Val Asp Gly Ala Val Ala Leu His Gly Leu Gly  
325 330 335

His Ala Tyr Glu Gly Val Glu Val Leu Ala Asp Ile Asp Leu Glu Leu  
340 345 350

Glu Asp Gly Ser Leu Val Ala Leu Val Gly Pro Ser Gly Ser Gly Lys  
355 360 365

Ser Thr Leu Leu His Leu Leu Ala Arg Tyr Met Asp Ala Gln Arg Gly  
370 375 380

Glu Leu Glu Val Gly Gly Leu Ala Leu Lys Asp Met Pro Asp Ala Val  
385 390 395 400

Arg His Arg His Ile Ala Leu Val Gly Gln Gln Ala Ala Ala Leu Glu  
405 410 415

Ile Ser Leu Ala Asp Asn Ile Ala Leu Phe Arg Pro Asp Ala Asp Leu  
420 425 430

Gln Glu Ile Arg Gln Ala Ala Arg Asp Ala Cys Leu Asp Glu Arg Ile  
435 440 445

Met Ala Leu Pro Arg Gly Tyr Asp Ser Val Pro Gly Arg Asp Leu Gln  
450 455 460

Leu Ser Gly Gly Glu Leu Gln Arg Leu Ala Leu Ala Arg Ala Leu Leu  
465 470 475 480

Ser Pro Ala Ser Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp  
485 490 495

Pro Gin Thr Ala Arg Gln Val Leu Arg Asn Leu Arg Glu Arg Gly Gly  
500 505 510

## 09743PC.ST25.txt

Gly Arg Thr Arg Val Ile Val Ala His Arg Leu Ala Glu Val Ser Asp  
 515 520 525

Ala Asp Leu Ile Leu Val Leu Val Ala Gly Arg Leu Val Glu Arg Gly  
 530 535 540

Glu His Ala Ala Leu Leu Ala Ala Asp Gly Ala Tyr Ala Arg Leu Trp  
 545 550 555 560

Arg Glu Gln Asn Gly Ala Glu Val Ala Ala  
 565 570

<210> 35  
 <211> 1725  
 <212> DNA  
 <213> *Pseudomonas aeruginosa*

<400> 35  
 atgaccctgt tcgaacgaat gcgtgcgtg cccgaagact gccgtgccgc gttgcgcgg 60  
 gcgagcgcct gggcggtcct ggcggcgctg ctggacgccc cttgcggcgt attgctggtg 120  
 ccgttggtcg aggccctggtt cgccgaaggc gcgttgcctt ggcgctgggt cgccgcgttg 180  
 ctcggcttga gcctggcgca ggcgctgttg cagtagctgg ccctgcgtcg cggttgcgc 240  
 gccggcggtcg ctgtggcgcc tggactggtg cgccgcctgg tggcgcgctt gccgcgcctg 300  
 gcgccgcggg cgctgcgcgg ggtcgcgccg gccgaaggcc tgctgcgcgg cccgggtatg 360  
 caggcgatgg gcattccggc gcacccgtcg gggccgcgtga tcgcccgcgtt ggtgacgcgg 420  
 ctcgggggtga tcctcggtct gttccctgatc gacccgttcca tcgcccctcg cctgctccctt 480  
 gctgggtgcct tcctcgccgc gctgttgcgc tggagcgggc ggcgaatct ggccggcgag 540  
 gatgcccggc tggccgcggc ggcgcacgcgc gcacggcagt tgcaggcggtt cgccgaacgc 600  
 cagccactgc tgccgcgcggc gcagcgcgaa agcgtcgccc gccaggggct ggaagaggcc 660  
 ttgcgcagtc tccaccgcag caccctggat ctgttgcggc gcacccgttcca cagccgcctc 720  
 ggcttcgcggc tggcggtgca ggcggcggttc gccttcgcggc tgctcgccgg cgccctggcg 780  
 gtggagcggtc aatggctgga cggcgctcggtt ctgggtggccg tgctgggtgt gctgggtgcgc 840  
 ttcatcgagc cgctggccca gtcacccat ctgcaccagg cggtgcgcgg cgccctggcag 900  
 ggcgtggata ccctgctgcgtt ggttttcgcgc ctggctccgc tgccgcacccc cgagccggc 960  
 gagcggccgc acgacgcggc cctggcggtt gaggccgtgg aattgcgcctt ggaagatggc 1020  
 cgccgccttgc tcgaggacat ttccctgagg ctggagccgg gttcgctgaa cgtccctcgatc 1080  
 ggaccctccg gggccggcaa gagcagcctg ctggcgctgc tgccgcggct ctacgacgtc 1140  
 gatgccgggc gtgtcctgt gggtggcggtg gatatccgc ggttgagcga aacgaccctc 1200  
 gccggccagtc gtaacctggt gttccaggac aacggcctgt tccgcggcag cggtgcctgg 1260

## 09743PC.ST25.txt

aacctgcgca	tggcgcgagc	ggacgcccgt	ctcgaagcgc	tgcgcgagggc	ggcgccggcg	1320
gttggcctgc	tggaagagat	cgaggcctgg	ccgcagggtct	gggacacagcga	cgtcggtccc	1380
ggcggcgccgc	tgctgtccgg	cggccagcgg	caacgcctgt	gcctggctcg	cgggctgctc	1440
tcgacggcgcc	cgttgctgtct	gctcgacgag	cccaccgcca	gcctcgacgc	cggcagcggag	1500
gcgcaagggtgc	tgcgcagcct	gctcggttg	cgcggccggc	gcaccctgct	ggtagtgacc	1560
caccggccgg	cgctggcgcc	tcaggccgac	caggtactgc	tgctggagga	ggggcgccctg	1620
cgcctcagcg	gacttcacgc	cgatctgctc	gtccgggacg	actggtatgc	cggtttcgtc	1680
gggctggcgcc	gcgaggaaag	ttcccgcgacg	gtcgtggatc	gatag		1725

&lt;210&gt; 36

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas aeruginosa

&lt;400&gt; 36

Met	Thr	Leu	Phe	Glu	Arg	Met	Arg	Ala	Leu	Pro	Glu	Asp	Cys	Arg	Ala
1									10						15

Ala	Leu	Arg	Arg	Ala	Ser	Ala	Trp	Ala	Val	Leu	Ala	Ala	Leu	Leu	Asp
							20		25					30	

Ala	Ala	Cys	Gly	Val	Leu	Leu	Val	Pro	Leu	Val	Glu	Ala	Trp	Phe	Ala
								35	40				45		

Glu	Gly	Ala	Leu	Pro	Trp	Arg	Trp	Val	Ala	Ala	Leu	Leu	Gly	Leu	Ser
							50	55				60			

Leu	Ala	Gln	Ala	Leu	Leu	Gln	Tyr	Leu	Ala	Leu	Arg	Arg	Gly	Phe	Ala
							65	70		75			80		

Ala	Gly	Gly	Ser	Leu	Ala	Ala	Gly	Leu	Val	Arg	Ser	Leu	Val	Ala	Arg
							85		90			95			

Leu	Pro	Arg	Leu	Ala	Pro	Pro	Ala	Leu	Arg	Arg	Val	Ala	Pro	Ala	Glu
							100		105			110			

Gly	Leu	Leu	Arg	Gly	Pro	Val	Met	Gln	Ala	Met	Gly	Ile	Pro	Ala	His
							115	120			125				

Leu	Leu	Gly	Pro	Leu	Ile	Ala	Ala	Leu	Val	Thr	Pro	Leu	Gly	Val	Ile
							130	135		140					

Leu	Gly	Leu	Phe	Leu	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Gly	Leu	Leu	Leu
							145	150		155		160			

## 09743PC.ST25.txt

Ala Gly Ala Phe Leu Ala Ala Leu Leu Arg Trp Ser Gly Arg Arg Asn  
165 170 175

Leu Ala Ala Glu Asp Ala Arg Leu Ala Ala Glu Arg Asp Ala Ala Arg  
180 185 190

Gln Leu Gln Ala Phe Ala Glu Arg Gln Pro Leu Leu Arg Ala Ala Gln  
195 200 205

Arg Glu Ser Val Ala Arg Gln Gly Leu Glu Glu Ala Leu Arg Ser Leu  
210 215 220

His Arg Ser Thr Leu Asp Leu Leu Arg Arg Ser Leu Pro Ser Gly Leu  
225 230 235 240

Gly Phe Ala Leu Ala Val Gln Ala Ala Phe Ala Phe Ala Leu Leu Gly  
245 250 255

Gly Ala Trp Ala Val Glu Arg Gln Trp Leu Asp Gly Ala Arg Leu Val  
260 265 270

Ala Val Leu Val Leu Leu Val Arg Phe Ile Glu Pro Leu Ala Gln Leu  
275 280 285

Thr His Leu Asp Gln Ala Leu Arg Gly Ala Trp Gln Ala Leu Asp Thr  
290 295 300

Leu Leu Arg Val Phe Ala Leu Ala Pro Leu Arg Ser Pro Glu Pro Gly  
305 310 315 320

Glu Arg Pro His Asp Ala Ser Leu Ala Ala Glu Ala Val Glu Leu Arg  
325 330 335

Leu Glu Asp Gly Arg Ala Leu Leu Glu Asp Ile Ser Leu Arg Leu Glu  
340 345 350

Pro Gly Ser Leu Asn Val Leu Val Gly Pro Ser Gly Ala Gly Lys Ser  
355 360 365

Ser Leu Leu Ala Leu Leu Gly Arg Leu Tyr Asp Val Asp Ala Gly Arg  
370 375 380

Val Leu Leu Gly Gly Val Asp Ile Arg Arg Leu Ser Glu Thr Thr Leu  
385 390 395 400

Ala Ala Ser Arg Asn Leu Val Phe Gln Asp Asn Gly Leu Phe Arg Gly  
405 410 415

## 09743PC.ST25.txt

Ser Val Ala Trp Asn Leu Arg Met Ala Arg Ala Asp Ala Asp Leu Glu  
420 425 430

Ala Leu Arg Glu Ala Ala Arg Ala Val Gly Leu Leu Glu Glu Ile Glu  
435 440 445

Ala Trp Pro Gln Gly Trp Asp Ser Asp Val Gly Pro Gly Gly Ala Leu  
450 455 460

Leu Ser Gly Gly Gln Arg Gln Arg Leu Cys Leu Ala Arg Gly Leu Leu  
465 470 475 480

Ser Thr Ala Pro Leu Leu Leu Asp Glu Pro Thr Ala Ser Leu Asp  
485 490 495

Ala Ala Ser Glu Ala Gln Val Leu Arg Ser Leu Leu Gly Leu Arg Gly  
500 505 510

Arg Arg Thr Leu Leu Val Val Thr His Arg Pro Ala Leu Ala Arg Gln  
515 520 525

Ala Asp Gln Val Leu Leu Leu Glu Glu Gly Arg Leu Arg Leu Ser Gly  
530 535 540

Leu His Ala Asp Leu Leu Val Arg Asp Asp Trp Tyr Ala Gly Phe Val  
545 550 555 560

Gly Leu Ala Gly Glu Glu Ser Ser Ala Thr Val Val Asp Arg  
565 570

<210> 37  
<211> 558  
<212> DNA  
<213> Pseudomonas aeruginosa

<220>  
<221> misc\_feature  
<222> (85)..(85)  
<223> Unknown nucleotide

<220>  
<221> misc\_feature  
<222> (88)..(88)  
<223> Unknown nucleotide

<220>  
<221> misc\_feature  
<222> (174)..(175)  
<223> Unknown nucleotide

09743PC.ST25.txt

```
<220>
<221> misc_feature
<222> (245)..(245)
<223> Unknown nucleotide
```

```
<220>
<221> misc_feature
<222> (293)..(293)
<223> Unknown nucleotide
```

```
<220>
<221> misc_feature
<222> (319)..(319)
<223> Unknown nucleotide
```

```
<220>
<221> misc_feature
<222> (325)..(325)
<223> Unknown nucleotide
```

<400> 37 ctcttcagc cgacacgcggc gcacacctgtg tgtgatcagt gagtggttg caactgcggg 60 tcaaggatct ggatttccct cacangtncg atcatcggtgc gggagggcaa gggctccaag 120 gatcgggcct tggatgttacc cgagagcttg gcacccagcc tgcgcgagca gggnnnaattg 180 atccgggttga tgaccctttt aatgacccctt aatagattat attactaatt aattggggac 240 cctanaggc ccctttttta ttttaaaaaat ttttcacaa aacggtttat ttncataaaag 300 cttgctcaat caatcacccnt atccncggga attcggccta ggcggccaga tctgatcaag 360 agacagaccc cttagctttgc atccggagcg accacacgag cgaggtcagt cactttcatc 420 gaagggaaattt tcttgacata gatctcacca cttccatgt cctcaaaggc atgccacact 480 aactcgacgc cttccctccaa agaaatcatg aaccgggtca tccgctcatc agtgataggc 540 aagacgcctc tgtcccttg 558

<210> 38  
<211> 479  
<212> DNA  
<213> *Klebsiella* sp.

```
<400> 38
acgcaggata tcttcttcat caaatgtcg atgcccgcct tcgctacgct gcggtttcag 60
tagaccgtaa cgacgctgcc aggcgcgcag tgtgaccgga ttgattccgc aacgttcggc 120
gacttcacccg atactgtaaa acgccatagc agcctcacat caacctgata ccttaatacc 180
taaactaacg aattcaggca tcctgtacaa ctctatttc ttgtacagat aaagatata 240
ggttgcggct cacagcgccc gggaaaaaaag atgaaaaaaat gttagctga ttgcgggtg 300
gttcatttt tctccggcca tgcgacggcg gtaggcggcc ccagggcgcg cgtggcgaac 360
```

## 09743PC.ST25.txt

aaattgccct	gaaactgtga	aataccggct	gattccagcc	acatccactc	ttcagcacgc	420
tcaacgccga	cggctgagac	cgcaatctcc	agagaagtac	agcatttgat	aatgcctg	479

<210> 39  
 <211> 516  
 <212> DNA  
 <213> Klebsiella sp.

<400> 39	gaccatgtgc	tgatgaccaa	taccgcctat	gagccaagcc	aggacttttg	tacaaaatt	60
ctcgccaaac	tcggcgtcac	caccagctgg	ttcgatccct	taatcggcgc	cgatatcgcc		120
cgtctggttc	gccctgagac	ccgcgtggtg	ttcctcgaat	cgcccggtc	gatcaccatg		180
gaagtgcacg	atgtgccggc	gatagtcgcc	gccgtgcgtc	aggtcgcccc	ggaagcgatt		240
atcatgatcg	ataacacctg	ggcggcgggg	atcctgttta	aagccctgga	ttttggcatt		300
gatatttcca	ttcaggcagg	caccaaatac	ctgatcggcc	attccgacgc	catggtgggc		360
accgcggtgg	cgaacgcgcg	ctgctggccg	cagctgcgtg	aaaatgccta	cctgatgggg		420
caaatgctgg	acgcccatac	tgcctatatg	accagccgcg	gcctgcgaac	cctggcggtg		480
cgccctgcgtc	agcatcatga	aagcagcctg	cgcata				516

<210> 40  
 <211> 377  
 <212> DNA  
 <213> Klebsiella sp.

<400> 40	cttttggccc	ctttttgtc	tttattctgg	agaacttatt	atggcggaaag	aatttggtcg	60
cccgcagcgt	gtggcccagg	agatgcaaaa	agagattgcc	atcatcctgc	agcgtgaaat		120
taaagatccg	cgtctggca	tgatgaccac	cgtttccgtt	gtggaaatgt	cccggtacct		180
ggcctatgcc	aaggtgtatg	tcaccttcct	taacgacaaa	gatgaagccg	cggtgaaagc		240
gggcataaaa	gcgcgcagg	aagcttctgg	ctttatccgc	tctctgctgg	ggaaagcgat		300
gcgtctgcgc	atcgtaaccgg	aactgacttt	cttctacgac	aactcactgg	tggaagggat		360
gcgtatgtcc	aacctgg						377

<210> 41  
 <211> 625  
 <212> DNA  
 <213> Klebsiella sp.

<400> 41	gcccagcccg	cttccccgt	tgcccagtta	aaagccttcg	tggagcagga	atttgctcag	60
attaagcatg	ttctgcacgg	catcagcctg	ctgggtcagt	gcccggacag	cgtcaatgcc		120
gcgcgtatct	gccgcggcga	aaagctctcc	atcgccatca	tggcgggtct	gctggaagcc		180
cgtggacaca	aagtcaagtgt	cattaacccg	gtcgaaaaac	tgctcgccgt	gggtcactat		240

09743PC.ST25.txt

ctggaaatcca ccgtcgatata cgccgaatcc acccgccgca ttgccgcccag ccagatcccg 300  
gcagaccata tgatcctgat ggccgggttt accgcccggca atgagaaaagg cgagctggtg 360  
gtgctggggc gtaacggctc cgactactcg gctgcggta c tggccgcctg cctgcgcgct 420  
gactgctgac aaatctggac cgatgtcgac ggagtgtaca cctgcgatcc gcgtcaggta 480  
ccggatgcgc gcctgctgaa atcgatgtct tattcaggagg cgatggagct ctcctacttt 540  
ggcgcgaaag tgctgcaccc ggcgcaccatt gcccctatcg cccagttcca aatcccatgc 600  
ctgattaaaa ataccggcaa ccccc 625

<210> 42  
<211> 355  
<212> DNA  
<213> *Klebsiella* sp.

```
<400> 42
ggcgcagcgt ctgctcgta ccgtcaagct cgaagcttaa cattgcgccaaaacctttt
gctgacgcgc cgcaatttca tgccctgggt tttccggcag cgatggatgatcacagcttt
tcaccagcggttggcttgcagatactcaa cgatcgccag ggcatttcgc tgcgccactt
ccatccgtgg agacagcgtc cgccgcgcaacacagcag atagctgtcg aaggcgctgc
cggtgacgcc aatatttattc gcccaccatg ccagttcggt gacagttgcc ggatctttgg
caatcaccac cccggccacc acatcgaggat gaccattgag gtatttggta cagga
355
```

<210> 43  
<211> 500  
<212> DNA  
<213> *Klebsiella* sp.

<400> 43 gttgcgtccc aggccggtaa acgcattcctg caggtagtca atttcgtcgt cggccagcgc 60  
cagaccaga cggagggttgg cgtcaatcag cgcctgacgc cttcgccca gcaggtcgac 120  
gctgggtgacc ggcgtcggct gatggtgagc gaacagcttc tcgcccgtt ccagctcgac 180  
gaagacgctc tccatcatgc ggtcatgcag ctccggcc accggggccc actgcgcttc 240  
ggtcagggtt gaggcttcaa cgtaatacgc cacgcccgc tcaagacgca caacctgcgc 300  
cagaccgcag ttgtgagcga tatcggttagc tttagaagac cagggagaga tggtgccagg 360  
gcgaggggtc acgagcagta atttaccggc cgggtatgg ctgcttaagc tcggggccata 420  
ctgaagcagt cgcgccaggc gtcgcgcata gtcagcgctc agcggggcgt tcagatcgcc 480  
aaaatgaata tattcggcat 500

<210> 44  
<211> 439  
<212> DNA  
<213> *Klebsiella* sp.

## 09743PC.ST25.txt

&lt;400&gt; 44

gtattggcat cgtactcctg ggctggccgg tgacaaaaggc gatgcgccta tctttgctgg	60
cgaacaaaata cgcacatcgccc tcttccgtct ccgcgaggat ctcgagatcg gtatagtcgc	120
gaataagtcc ggccggaaaa tcagcatagc gtgagtgccg ggcaggaaa gagtcgtcga	180
aaccgcgggt cagtaaggcg tgccgatgaa gaatatggtg ttcatagacg .ccggaaatct	240
tttcggcgcg ggtctgcttg ggaatgccgt acagaatgtt cagcgcggcc tgaaccgccc	300
aacagacgaa cagcgtcgaa gtgacgtgat cttggccca ctccagcacc tgtttgcgtct	360
gcggccagta agcaacatcg ttaaactcaa ccaggcctaa aggagcgcgg gtaacaatca	420
ggccgtcaaa gttctgatc	439

&lt;210&gt; 45

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

&lt;400&gt; 45

gaggttcata tgtccgtact cgatctaaac gcgcctaattg cattgccgaa agtggAACgc	60
attctggcac tcgcggaaac caacgcccac ctggaaaagc ttgacgccga agggcgtgtg	120
gcgtggcgc tggaaaatct gccggaaac tatgtgctgt cgtcgagctt tggcattcag	180
gcggcggtaa gtttgcatact ggtgaatcag atccgcggg acattccggt gatcctcacc	240
gataccggct acctgttccc ggaaacctat cagtttattg acgagctgac ggacaag	297

&lt;210&gt; 46

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

&lt;400&gt; 46

tgttaaagcg tgcgttctac agcctgttag tcctgctcgg cctgctgctg ttgaccgtgc	60
tgggccttga ccgctggatg agctggaaaa ccgcgccta tatctatgtt gaactgcagg	120
acctgcctta ccgtcaggc ggtgtggc tgggcaccgc caaatattac cgcaccggcg	180
tcatcaatca gtattaccgt taccgcattcc agggcgcgtt gaacgcctac aacagcggca	240
aggtaacta tctcctgctg agcggcgata atgctctgca aagctacaat gaaccgatga	300
ccatgcgtcg ggacctgatt aaaggcggcg tcgatcccgc ggatatcgta ctggactatg	360
ccggtttccg taccctcgac tcgatcgatcc gtacccggaa agtgttcgac accaacgact	420
tcattatcat caccctcgac ttccactgatcc aacggcgctt gtttatcgcc ctgcataatgg	480
ggatccaggc ccagtgcgtac gc	502

&lt;210&gt; 47

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

09743PC.ST25.txt

&lt;400&gt; 47

cgctgaacct cctcaaacaa acgcaggccc tgcacctgtc ggctgcaggg gaccagcgtg	60
gatccgctca aacagctgca ggccgagcac cttctcaaag cgccgcagct cgccgctgac	120
cgtgggttgc gaggtgtgca gcatccgcgc cgcttcggtc aggttgcgg tggtcatcac	180
cgcgtgaaag atttcgatatacgcaatt gacggctggc atgcggtctc cgtgaggctc	240
ggctggaacc atatcatttt tgcatagagt cgcgataaaaa cgatattttt tattcgtctg	300
tcactgtggc gtaatcagaa aaaacacgcga ccaacacacg cactgcaccc gagttcttat	360
gccacactcg ctttacgcca ccgatactga cctgaccgcg gacaacctgc tgcgcctgcc	420
ggcgaaattt ggctgcccgg tctgggtcta tgatgcgcag attattcgcc gccagatagc	480
ccagctcagc cagtttcgac	500

&lt;210&gt; 48

&lt;211&gt; 229

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

&lt;400&gt; 48

ggcttccacc caaatcgctt tgcggcaac gatTTTgct aaaacggctt tgcattctt	60
accctcttgc ccgctaagtgcggtcactctgtcataggccgcgcgcgtgc tgcagcacat	120
ccagtacctg ctgagcgtta gctttcagat cttcatgccc gtgtaaacgc atcaatatgg	180
cgacgttggc ggcgacggcg gcttcgtgag cggcttcacc tttaccttg	229

&lt;210&gt; 49

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

&lt;400&gt; 49

tggctcaacgcg ctgctcagtg gtgcgagggtgcactttggatcacatcg gcgttgtctgcacagtggaaa tcagatccag cgccgcgtcc gtttacgc acgtagtccg gattgtgggt	60
gcctttctta acgatattca gacccggccc ttccgagatgc agggccagcg cctgggttcggatgttttgc agatattcgc gcatcacgcg cacgccttgc ttcatcagat cgtcgctgga	120
ggtaatcagc gtcggcagga agctggtgca gcctgagcgt tcgttggct tctgcattgtatctccagcggtt tcgacagtga ccgcctctgg gctgtcgat aactgcacgc cgccgcagcc	180
gtttagctgg acgtcgataa aaccgggggc gattattgcg ccgttgactg agcgctgctcgatgtcagac ggcaaatctgc cagcggaca aagacgttgcg ataaag	240
	300
	360
	420
	466

&lt;210&gt; 50

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Klebsiella sp.

## 09743PC.ST25.txt

<400> 50  
 ttaagcacca tatcgtaaccg ctgctggcgc agcgtctgaa tgagctgccaa ttgcataatcc 60  
 agctgataacc ttttccctg gcttttcca gcggcgatcg agaccataaa tatgggtggat 120  
 atcgggggttg gctgcgagca tatcccgggt ctcttcataac aacaggacat ccacgctggc 180  
 ggccgggtac tgctgtttca gcgctgaat aagcggcgtg atcagcagca tgtcgcccatt 240  
 atggcgcagc ttaatgacca ggatccgcgc cgggttcaac gggccgcggg agagggtttc 300  
 aggcgctata ctctgttctt catccaggat aagggttccg attctagggg atcagacaga 360  
 ttgagagaag cgttgtattt ctctaccatg acccgataacg tatggcctga ggacgtttc 420  
 gtgcacaatc ccgcaatttc tcatacagat 450

<210> 51  
 <211> 450  
 <212> DNA  
 <213> Klebsiella sp.

<400> 51  
 cactcaggct tgcctgttaac gcttggcgc catcacgtaa ggctgtatcg aaaataatga 60  
 cttgctggct catggtttgg atccttagtc tgggtccctgg cgccttggat acgagcataaa 120  
 aaaaacccgc gccaaggcgc gggtttata gtcttgctgg aagatgactt aacgctgaac 180  
 gtcgcccac acgctaccga gcaaattggca tgcgtttagt agtagtaggc tggtgatacg 240  
 agcggtgca atcattgcgt caaactccag atgaaatcgt tatgcttttta gagttactgg 300  
 atagccgttt taaaatcaac ccctggcatg gaaaaagcgt tttggctga ctaaatgaat 360  
 tagcaaaaatg tgctgtatgt a gccccatggat tgccgaagat cctatggat accgaaggcg 420  
 gtttatcccc aatttggatcc atttgaaaaaa 450

<210> 52  
 <211> 575  
 <212> DNA  
 <213> Klebsiella sp.

<400> 52  
 cgctgaaccg ctatccggag ccgcagccga agtgcgtga ttgagagcta cgcccgctac 60  
 gcccgggtca aaccggagca ggtgctggtc agccgcggcg ccgacgaagg catcgagctg 120  
 ctgatccgcg ctttctgtga gcccggcgaa gacgcgggtc tctactgccc gccgacctac 180  
 ggcatgtaca ggcgtcagcgc cgagaccatc ggcgtcgagt gcccgcaccgt gccgacgctg 240  
 gccagctggc agctcgacct gcccggcatc gaagcgcggc tggacggcgt gaaggtggtg 300  
 tttgtctgca gcccgaacaa cccgaccggg cagattatcg acccgagtc gatgcgcgac 360  
 ctgctggaga tgaccgcgg caaagccatc gtgggtggccg acgaaggccta tattgaattc 420  
 tgcccgccagg cgacgctcgc cggctggctc agcgactatc cgcacctgggt ggtgctgcgc 480

## 09743PC.ST25.txt

acgctgtcca aagccttcgc cctcgccggc ctgcgtcg	gcttcaccct cgccaa	cgcc	540
gaggtgatta acgtgctgct gaaagtgatc gcccc			575

<210> 53  
 <211> 375  
 <212> DNA  
 <213> Klebsiella sp.

<400> 53			
cgtatatttc atcgtacaga aaccgtaaac acaggcattg	gctgatttc	agtgagtgaa	60
tttaaataga cttctgccgt tttcaatgct tcggcgatgg	tcacatccat	atcaaggtaa	120
cggtaggttc caagacgacc gacaaaagtg atgttggttt	cattctcg	caatgacaaa	180
tattttcaa gaagagccat ttctccatc tggcgaatag	gatagtaagg	aatatcattt	240
tcttcacaag cacggctata ctctttataa caaacagagc	cgtcg	ttccaggga	300
gaaaaatatt tatgttcagt gatgcgagta tagggcacat	ccacagaaca	gtagttcattc	360
actgcgcattc cctgg			375

<210> 54  
 <211> 400  
 <212> DNA  
 <213> Klebsiella sp.

<400> 54			
gtaccccgat tttatatgct tctgatatga ttccggaaaa	atttagctgg	ataattacct	60
acaatccgct agcgagtatg attcttagtt ggcgtgattt	attcatgaat	gggactctta	120
atttttagta tatttctata ctctatTTTA	cgggaattat	tttgacggtt	180
ctatTTTCAA taaattaaaa tatcgatttg cagagatcta	aaagtgcgt	ataagagcag	240
catgctaggc tatttatggt cagtagcaa tccattgctt	tttgccatga	tttactatTTT	300
tatatttaag ctggtaatga gagtacaaat tccaaattat	acagtttcc	tcattaccgg	360
cttggTTCCG tggcaatggc ttggccagttc ggccactaac			400

<210> 55  
 <211> 413  
 <212> DNA  
 <213> Klebsiella sp.

<400> 55			
cgagccaccc actgtagcgt atggatatcg cgcaagccgc	cggggctgct	tttcacgtcc	60
ggctcgaggt tatacgctggt gccatgatag cgctgatgac	ggacgttctg	ctcttcgacc	120
ttggcggcga agaacttttc cgatggccag aagccgtcgc	taaaaaatatg	tttttgcagt	180
tcaaggaaca gcgacgtc gcccgtcagc aggccgtcatt	cgatTAAGTT	ggggcaacg	240
gtcagatccg agagaccttc cagcaggcac tcttcgaggg	tgcgtacgct	gtggcccacc	300
tccagcttga cgtcccacag cagggtgagc agttccggca	cttttgcgc	ctggcgtcc	360

## 09743PC.ST25.txt

ggcagtttt tacgactgag gatcagcaga tcgacgtctg agagcgggtg cag 413

<210> 56  
<211> 500  
<212> DNA  
<213> Klebsiella sp.

<400> 56  
cttaacccgc acgctggcga aggcggccat atggaaacag aagagataga caccatcatt 60  
ccggtgctgg aagagatgctg cgcaaagggg atgaacctca gcggtccgct gccggcagac 120  
actctcttgc agccgaaata tcttgatcat gccgatgcgg tactcgcgat gtaccacgat 180  
cagggcctgc ccgtgctaaa ataccaggc tttggccgct gcgtgaacat tacgctcggt 240  
ttacctttta ttcgtacctc cgtcgaccac ggcaccgcac tggaaattgc gggccaggga 300  
aaagcggacg tcggcagttt tatcacggcg cttaatctcg ccatcaaaat gattgttaat 360  
acccaatgaa taatcgagtc catcagggcc atttagcccg caaacgcttc gggcagaact 420  
tcctcaacga tcagttgtg atcgacagca tcgtctcgcc gattaacccg cagaaaggcc 480  
aggcgatggt tgaaatcgcc 500

<210> 57  
<211> 473  
<212> DNA  
<213> Klebsiella sp.

<400> 57  
gggtctgacc cccgttctgt gcatcggtga aaccgaagcc gaaaacgaag cgggcaaaac 60  
ggaagaagtt tgcgcacgtc agatcgacgc cgtgctgaaa acccaggcgctt 120  
cgaaggcggtg gttatcgctt acgaaccagt atgggctatc ggtaccggca aatcagcgac 180  
cccggtctcg ggcgaggcg 240  
tgcacaaatt catccgtgac cacattgcta aagctgacgc 240  
caaaatcgct gagcaagtga tcatccagta cggcggttcc gttaacgctg gcaacgcccgc 300  
agagctgttc acccagccgg acatcgacgg cgcgctgggtt ggcggcgctt ccctgaaagc 360  
tgacgcttgc gccgtgatcg tttaaggcgc agaaggcagcg aaaaaaggcgt aattcgctt 420  
tccccgtggc gacacgac 473  
cggtttgact gacaaaacgt gggagcccg cct

<210> 58  
<211> 463  
<212> DNA  
<213> Klebsiella sp.

<400> 58  
ggtggcgac cctggcgatcg tttgtttaga aattatgaat attaataccaa gaaaaattcc 60  
taatttttgcgtacgctctg acgagcgac aataaaacaa gacgaatttt tgaacaattg 120  
tctttaaatt tgtaatttgc attgatctgt tggtgtttaa aggtatttgc atttcttttgc 180

## 09743PC.ST25.txt

tatagatatg taaattaaca ttgaaaagcc	atttcaaaaa ttaaatatat ggcgaacata	240
gctattaact tatagttaac atcttcccg	gttgccttt gataacttcgg gtaatataatt	300
tatTCGcac atcaaataa ctcttttc ttctgttgt	tattcatggc catctattgg	360
cggaaataagg cagagtagag ggggatgtgc	ctaatacct gcggaaggaa cgcaatgtac	420
atttacaggg aggagctgac gagccgttc	gcgatagctt tag	463

<210> 59  
 <211> 526  
 <212> DNA  
 <213> Klebsiella sp.

<400> 59		
ttgggttgt gctcgcaag aaatttaatc	tgccggcat cgtaagttt gttggcgg	60
gaagagtatt ttcttctgac agcatgcctt	taaaattatt gcggcagttt actattgctg	120
catataaaata tattgccagt aataagcgct	gtatatttat gttgaacat gaccgcgaca	180
gaaaaaaaaact ggctaagttg gttggactcg	aagaacaaca gactattgtt attgatggtg	240
caggcattaa tccagagata tacaaatatt	ctcttgaaca ggatcacgat gtccctgttg	300
tattgtttgc cagccgtatg ttgtggagta	aaggactggg cgacttaatt gaagcgaaga	360
aaatattacg cagtaagaat attcaattta	ctttgaatgt tgctgaaatt ctggcgaaa	420
atgataaaga tgcaatttcc cttcagggtc	attgaaaatt ggcatcagca aggattaatt	480
aactggtag gtcgttcgaa taatgtttgc	gatcttattt agcaat	526

<210> 60  
 <211> 473  
 <212> DNA  
 <213> Klebsiella sp.

<400> 60		
ttacttgccc cttttgccc aactgaaaca aaggcccgtg	ctggtgatcg gcggcgccgaa	60
gattgctgaa cgtaagatca agttcctgct	gcgcgcggcag gcgcagggtgc aggtggcgc	120
tgaaacgctg tcaccggcgc tggccgatct	ggctgcgcgc caggcactca gctggcgccg	180
gacggcattc agcgactcgc tggtgatga tgcgtttctg	gtgattgcgg ccaccgagga	240
tgaggcgctt aaccagcggg tggccgcgc	agctaacgcg cgctaccggc tggtaacgt	300
ggtgataac caggcgctgt	gctcggtttgt tttcccttct atcgatcgacc gttcgccgct	360
gctggcgatc atctcctcca	gcggtaaagc gccgggttg tcgcgcattc tgcgtgaaaa	420
aatcgaagcg ctgctgccga	cgaatctcg tcggctggcg gaatcagcaa gct	473

<210> 61  
 <211> 451  
 <212> DNA  
 <213> Klebsiella sp.

## 09743PC.ST25.txt

<400> 61  
 agcaggggcaa tggtgtcgg tttcataaca tttcctgatg atgaaaagtca tattaaccgg 60  
 cattctaaaca gcagcattca gaggggcaat gatttggc aaccgattac gacgatcgcc 120  
 gcaaatgcta aaaaagggag aggggattac cagctggcgg gctttccgc gccgagatta 180  
 tccagcacgg cgcgacgcgc caggccgtca ggaaagtcaa ggtccggggc gatctgaac 240  
 agcggccaga gcataaagcc gcggttttc atatcgtagt gcggaacggg caggcgctcg 300  
 ctgttaatga cagcatcgcc aaacagcatg atatcgaggt ccagcgtgcg cggcccccag 360  
 cgttcggctt tgccgactcg cccctgctgc agttcgatgc gctgagtagt atcgagcagc 420  
 gtctcggggg gcagggcggt ttccagcgca a 451

<210> 62  
 <211> 525  
 <212> DNA  
 <213> Klebsiella sp.

<400> 62  
 ggcttaacgc cagctatgtc aacgctgcgg ttatgcggat ttttcatgcc tctgcggcta 60  
 acagaaaaaa gccttatgtat agctatacta atggggctt ttactccgtt ttgaccggat 120  
 tcctgaccgg cgtcagggtc aagtacaaaa aatcatcaca atttccgtc accggcgcta 180  
 caatcgaccg aagtacacaat ctcaaatacg aagagtattg ctaatgaaaa acatcaaccc 240  
 aacgcagacc tctgcctggc aggcattaca gaaacacttc gacgaaatga aagatgtcac 300  
 tatcagcgag ctttcgcca aagatagcga ccgttttct aaattttccg cgacgttcga 360  
 cgatctgatg ctgggtggact tctccaaaaa ccgcatcact gaagagacgc tggctaaact 420  
 . gcaggatctg gcaaagaga ctgacctggc gggcgctatc aagtcgatgt tctcaggtga 480  
 gaagatcaac cgacccgaag accgcgcggg actgcacgtc gcgc 525

<210> 63  
 <211> 475  
 <212> DNA  
 <213> Klebsiella sp.

<400> 63  
 tgcttcatcc gcatctcctt gaaatttatt tggtcttagg cggacggtag agcgctaata 60  
 gctcgccac cttttacgc gtaccaccgt tgctgctgtat gctgcgcgc accttcacaa 120  
 tatcggtttc tgccgcgttt ttataccatt cctgcgtcag cggcgtgcgg tggttggaaa 180  
 tcagcaccgg gatgcgtttt ttcatcagcg attccgcctt ttgcgcgcagc agtacctgtt 240  
 gttccaggtt gaaactgttg gtgtggtagg cggtaaagt cggcgccgc gttagcggcg 300  
 catagggcgg atcgcaatac accactgtgc ggctatccgc acgttgcatt cactcttcgt 360  
 aagattcgca gtaaaaactcg gcgtttgcg ctttcggc gaaatgatag agtcagctt 420  
 cggggaaata gggctttta taacggccaa acggcacatt gaactcgccg cgcc 475

## 09743PC.ST25.txt

<210> 64  
<211> 286  
<212> DNA  
<213> Klebsiella sp.

<400> 64  
tgtcaatgcg caatttggtt aaatatgtcg gtattggcct gctggtgatg gggcttgccg 60  
cctgcgataa cagcgattca aaagcgccaa ccgttggcgc agcagcggag agcaatgcca 120  
gcggccaggc aatcagcctg ctggatggca agctgagctt caccctgcct gcgggcattgg 180  
ccgaccagag cggcaaactg ggtacccagg cgaacaatat gcacgtctac tctgacgcta 240  
ccggccagaa agcggtcatc gtcatcgctcg gcgacagcac caatga 286